

SEQUENCE LISTING

<110> TOMLINSON, Stephen  
HOLERS, V. Michael

<120> Complement Receptor 2 Targeted  
Complement Modulators

<130> 577712000200

<140> US 10/534,772  
<141> 2003-11-13

<150> PCT/US2003/036459  
<151> 2003-11-13

<150> US 60/426,676  
<151> 2002-11-15

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 1041  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 1  
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tttcccgagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 120  
gagaaggact cagtgatctg ccttaaggcc agtcaatggt cagatattga agagttctgc 180  
aatcgttagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 240  
actcagaatt atttccagt cggtactgtt gtggaaatatg agtgccgtcc aggttacaga 300  
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 360  
gtcgaatttt gtaaaaagaa atcatgcctt aatccgggag aaatacggaa tggtcagatt 420  
gatgtaccag gtggcatatt atttggtca accatctcct tctcatgtaa cacagggtac 480  
aaattatttg gctcgacttc tagttttgtt cttatttcag gcagctctgt ccagtggagt 540  
gaccgcgtgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgg 600  
ataattcaag gggAACGTGA ccattatgg tatagacagt ctgtaacgtt tgcatgtat 660  
aaaggatcca ccatgattgg agagcactt atttattgtt ctgtgaataa tgatgaagga 720  
gagttggatgt gcccaccacc tgaatgcaga ggaaaatctc taacttccaa ggtcccacca 780  
acagttcaga aacctaccac agtaaatgtt ccaactacag aagtctcacc aacttctcag 840  
aaaaccacca caaaaaccac cacaccaat gctcaagcaa cacggagttac acctgtttcc 900  
aggacaacca agcattttca tggaaacaacc ccaaataaaag gaagtggAAC cacttcaggt 960  
actaccgcgc ttctatctgg gcacacgtgt ttcacgttga caggtttgct tgggacgcta 1020  
gtaaccatgg gcttgctgac t 1041

<210> 2  
<211> 380  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 2

Met	Thr	Val	Ala	Arg	Pro	Ser	Val	Pro	Ala	Ala	Leu	Pro	Leu	Leu	Gly
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Glu	Leu	Pro	Arg	Leu	Leu	Leu	Leu	Val	Leu	Leu	Cys	Leu	Pro	Ala	Val
															20
Trp	Asp	Cys	Gly	Leu	Pro	Pro	Asp	Val	Pro	Asn	Ala	Gln	Pro	Ala	Leu
															35
Glu	Gly	Arg	Thr	Ser	Phe	Pro	Glu	Asp	Thr	Val	Ile	Thr	Tyr	Lys	Cys
															50
Glu	Glu	Ser	Phe	Val	Lys	Ile	Pro	Gly	Glu	Lys	Asp	Ser	Val	Ile	Cys
															65
Leu	Lys	Gly	Ser	Gln	Trp	Ser	Asp	Ile	Glu	Glu	Phe	Cys	Asn	Arg	Ser
															85
Cys	Glu	Val	Pro	Thr	Arg	Leu	Asn	Ser	Ala	Ser	Leu	Lys	Gln	Pro	Tyr
															100
Ile	Thr	Gln	Asn	Tyr	Phe	Pro	Val	Gly	Thr	Val	Val	Glu	Tyr	Glu	Cys
															115
Arg	Pro	Gly	Tyr	Arg	Arg	Glu	Pro	Ser	Leu	Ser	Pro	Lys	Leu	Thr	Cys
															130
Leu	Gln	Asn	Leu	Lys	Trp	Ser	Thr	Ala	Val	Glu	Phe	Cys	Lys	Lys	Lys
															145
Ser	Cys	Pro	Asn	Pro	Gly	Glu	Ile	Arg	Asn	Gly	Gln	Ile	Asp	Val	Pro
															165
Gly	Gly	Ile	Leu	Phe	Gly	Ala	Thr	Ile	Ser	Phe	Ser	Cys	Asn	Thr	Gly
															180
Tyr	Lys	Leu	Phe	Gly	Ser	Thr	Ser	Ser	Phe	Cys	Leu	Ile	Ser	Gly	Ser
															195
Ser	Val	Gln	Trp	Ser	Asp	Pro	Leu	Pro	Glu	Cys	Arg	Glu	Ile	Tyr	Cys
															210
Pro	Ala	Pro	Pro	Gln	Ile	Asp	Asn	Gly	Ile	Ile	Gln	Gly	Glu	Arg	Asp
															225
His	Tyr	Tyr	Arg	Gln	Ser	Val	Thr	Tyr	Ala	Cys	Asn	Lys	Gly	Phe	
															245
Thr	Met	Ile	Gly	Glu	His	Ser	Ile	Tyr	Cys	Thr	Val	Asn	Asn	Asp	Glu
															260
Gly	Glu	Trp	Ser	Gly	Pro	Pro	Glu	Cys	Arg	Gly	Lys	Ser	Leu	Thr	
															275
Ser	Lys	Val	Pro	Pro	Thr	Val	Gln	Lys	Pro	Thr	Thr	Val	Asn	Val	Pro
															290
Thr	Thr	Glu	Val	Ser	Pro	Thr	Ser	Gln	Lys	Thr	Thr	Thr	Lys	Thr	Thr
															305
Thr	Pro	Asn	Ala	Gln	Ala	Thr	Arg	Ser	Thr	Pro	Val	Ser	Arg	Thr	Thr
															325
Lys	His	Phe	His	Glu	Thr	Thr	Pro	Asn	Lys	Gly	Ser	Gly	Thr	Thr	Ser
															340
Gly	Thr	Thr	Arg	Leu	Leu	Ser	Gly	His	Thr	Cys	Phe	Thr	Leu	Thr	Gly
															355
Leu	Leu	Gly	Thr	Leu	Val	Thr	Met	Gly	Leu	Leu	Thr				
															370
															375
															380

<210> 3

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 3  
cagtgcata actgtcctaa cccaaactgct gactgcaaaa cagccgtcaa ttgttcatct 60  
gattttgatg cgtgtctcat taccaaagct gggttacaag tgtataacaa gtgttggaaag 120  
ttttagcatt gcaatttcaa cgacgtcaca acccgcttga gggaaaaatga gctaacgtac 180  
tactgctgca agaaggacct gtgtaacattt aacgaacagc ttgaaaatgg tgggacatcc 240  
ttatcagaga aaacagttct tctgctggtg actccatttc tggcagcagc ctggagcctt 300  
catccc 306

<210> 4  
<211> 126  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 4  
Met Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu Val Leu  
1 5 10 15  
Ala Val Phe Cys His Ser Gly His Gln Cys Tyr Asn Cys Pro Asn Pro  
20 25 30  
Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe Asp Ala  
35 40 45  
Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys  
50 55 60  
Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg Glu Asn  
65 70 75 80  
Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu  
85 90 95  
Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val Leu Leu  
100 105 110  
Leu Val Thr Pro Phe Leu Ala Ala Trp Ser Leu His Pro  
115 120 125

<210> 5  
<211> 1485  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 5  
atttcttgtg gctctcctcc gcctatccta aatggccgga ttagttatta ttctacccccc 60  
attgctgttg gtaccgtat aaggtagt tgttcaggtt ccttccgcct cattggagaa 120  
aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataaa acctgctcct 180  
aaatgtgaat attcaataa atattctct tgccttgagc ccatagttacc aggaggataac 240  
aaaatttagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 300  
aacttctcca tgaacggaaa caagtctgtt tgggtcaag caaataatat gtggggccg 360  
acacgactac caacctgtgt aagtgtttc cctctcgagt gtccagcact tcctatgatc 420  
cacaatggac atcacacaag tgagaatgtt ggctccattt ctccaggatt gtctgtgact 480  
tacagctgtg aatctggta cttgcttggt ggagaaaaga tcattaactg tttgtcttcg 540  
ggaaaatgga gtgtgtccc cccccacatgt gaagaggcac gctgtaaatc tctaggacga 600  
tttcccaatg ggaaggtaaa ggagccttcca attctccggg ttgggttaac tgcaaacttt 660  
ttctgtatg aagggtatcg actgcaaggc ccaccttcta gtcgggtgtt aattgtgttgg 720  
cagggagttt cttggaccaa aatgccagta tgggtggatgtt gggtgggtgg cggcggatcc 780  
gactgtggcc ttcccccaga tgcacctaattt gcccagccag ctttggaaagg ccgtacaatgtt 840  
tttcccgagg atactgtat aacgtacaaa tggtaagaaa gctttgtgaa aattcctggc 900

gagaaggact cagtatctg ccttaaggc agtcaatggc cagatattga agagttctgc 960  
aatcgtagct gcgagggtcc aacaaggcta aattctgcat ccctcaaaca gccttatatac 1020  
actcagaatt atttccagt cggtaatgtt gtggaatatg agtgcgcgtcc aggttacaga 1080  
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 1140  
gtcgaatttt gtaaaaagaa atcatgcct aatccgggag aaatacggaaa tggtcagatt 1200  
gatgtaccag gtggcatatt atttggtgca accatctct tctcatgtaa cacagggtac 1260  
aaattatttg gctcgacttc tagttttgt cttatbtcag gcagctctgt ccagtggagt 1320  
gaccgttgc cagagtgcag agaaattat tgtccagcac caccacaaat tgacaatgg 1380  
ataattcaag gggAACGTA ccattatgg tatagacagt ctgtaacgta tgcatgtaat 1440  
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<210> 6

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 6

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Tyr	Ser	Thr	Pro	Ile	Ala	Val	Gly	Thr	Val	Ile	Arg	Tyr	Ser	Cys	Ser
								20			25			30	
Gly	Thr	Phe	Arg	Leu	Ile	Gly	Glu	Lys	Ser	Leu	Leu	Cys	Ile	Thr	Lys
								35			40			45	
Asp	Lys	Val	Asp	Gly	Thr	Trp	Asp	Lys	Pro	Ala	Pro	Lys	Cys	Glu	Tyr
								50			55			60	
Phe	Asn	Lys	Tyr	Ser	Ser	Cys	Pro	Glu	Pro	Ile	Val	Pro	Gly	Gly	Tyr
								65			70			75	
Lys	Ile	Arg	Gly	Ser	Thr	Pro	Tyr	Arg	His	Gly	Asp	Ser	Val	Thr	Phe
								85			90			95	
Ala	Cys	Lys	Thr	Asn	Phe	Ser	Met	Asn	Gly	Asn	Lys	Ser	Val	Trp	Cys
								100			105			110	
Gln	Ala	Asn	Asn	Met	Trp	Gly	Pro	Thr	Arg	Leu	Pro	Thr	Cys	Val	Ser
								115			120			125	
Val	Phe	Pro	Leu	Glu	Cys	Pro	Ala	Leu	Pro	Met	Ile	His	Asn	Gly	His
								130			135			140	
His	Thr	Ser	Glu	Asn	Val	Gly	Ser	Ile	Ala	Pro	Gly	Leu	Ser	Val	Thr
								145			150			155	
Tyr	Ser	Cys	Glu	Ser	Gly	Tyr	Leu	Leu	Val	Gly	Glu	Lys	Ile	Ile	Asn
								165			170			175	
Cys	Leu	Ser	Ser	Gly	Lys	Trp	Ser	Ala	Val	Pro	Pro	Thr	Cys	Glu	Glu
								180			185			190	
Ala	Arg	Cys	Lys	Ser	Leu	Gly	Arg	Phe	Pro	Asn	Gly	Lys	Val	Lys	Glu
								195			200			205	
Pro	Pro	Ile	Leu	Arg	Val	Gly	Val	Thr	Ala	Asn	Phe	Phe	Cys	Asp	Glu
								210			215			220	
Gly	Tyr	Arg	Leu	Gln	Gly	Pro	Pro	Ser	Ser	Arg	Cys	Val	Ile	Ala	Gly
								225			230			235	
Gln	Gly	Val	Ala	Trp	Thr	Lys	Met	Pro	Val	Cys	Gly	Gly	Ser	Gly	
								245			250			255	
Gly	Gly	Gly	Ser	Asp	Cys	Gly	Leu	Pro	Pro	Asp	Val	Pro	Asn	Ala	Gln
								260			265			270	
Pro	Ala	Leu	Glu	Gly	Arg	Thr	Ser	Phe	Pro	Glu	Asp	Thr	Val	Ile	Thr
								275			280			285	
Tyr	Lys	Cys	Glu	Glu	Ser	Phe	Val	Lys	Ile	Pro	Gly	Glu	Lys	Asp	Ser
								290			295			300	
Val	Ile	Cys	Leu	Lys	Gly	Ser	Gln	Trp	Ser	Asp	Ile	Glu	Glu	Phe	Cys
								305			310			315	
															320

Asn	Arg	Ser	Cys	Glu	Val	Pro	Thr	Arg	Leu	Asn	Ser	Ala	Ser	Leu	Lys
				325				330						335	
Gln	Pro	Tyr	Ile	Thr	Gln	Asn	Tyr	Phe	Pro	Val	Gly	Thr	Val	Val	Glu
				340				345						350	
Tyr	Glu	Cys	Arg	Pro	Gly	Tyr	Arg	Arg	Glu	Pro	Ser	Leu	Ser	Pro	Lys
				355				360				365			
Leu	Thr	Cys	Leu	Gln	Asn	Leu	Lys	Trp	Ser	Thr	Ala	Val	Glu	Phe	Cys
				370				375				380			
Lys	Lys	Lys	Ser	Cys	Pro	Asn	Pro	Gly	Glu	Ile	Arg	Asn	Gly	Gln	Ile
				385				390			395			400	
Asp	Val	Pro	Gly	Gly	Ile	Leu	Phe	Gly	Ala	Thr	Ile	Ser	Phe	Ser	Cys
				405				410					415		
Asn	Thr	Gly	Tyr	Lys	Leu	Phe	Gly	Ser	Thr	Ser	Ser	Phe	Cys	Leu	Ile
				420				425				430			
Ser	Gly	Ser	Ser	Val	Gln	Trp	Ser	Asp	Pro	Leu	Pro	Glu	Cys	Arg	Glu
				435				440				445			
Ile	Tyr	Cys	Pro	Ala	Pro	Pro	Gln	Ile	Asp	Asn	Gly	Ile	Ile	Gln	Gly
				450				455				460			
Glu	Arg	Asp	His	Tyr	Gly	Tyr	Arg	Gln	Ser	Val	Thr	Tyr	Ala	Cys	Asn
				465				470			475			480	
Lys	Gly	Phe	Thr	Met	Ile	Gly	Glu	His	Ser	Ile	Tyr	Cys	Thr	Val	
				485				490					495		

<210> 7  
<211> 1002  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

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attgctgttgc gtaccgtat aaggtaactg tgttcaggtt ccttccgcct cattggagaa 120  
aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataaa acctgctcct 180  
aaatgtaat attcaataa atattctct tgccctgagc ccatagttacc aggaggatac 240  
aaaatttagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaaacc 300  
aacttctcca tgaacggaaa caagtctgtt tgggtgtcaag caaataatat gtggggccg 360  
acacgactac caacctgtgt aagtgtttc cctctcgagt gtccagcact tcctatgatc 420  
cacaatggac atcacacaag tgagaatgtt ggctccatttgc ctccaggatt gtctgtgact 480  
tacagctgtt aatctggtaa cttgttttttggagaaaatgc tcattaactg tttgtcttcg 540  
ggaaaaatgaa gtgtgttccc cccccacatgt gaagaggac gctgtaaaatc tctaggacga 600  
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttgggtgttaac tgcaaacttt 660  
ttctgtatg aagggtatcg actgcaaggc ccaccttcta gtcgggtgtt aattgtgttgg 720  
cagggaggatg cttggaccaa aatgccatgt tgttcaggag gaggaggatc cctgcagtgc 780  
tacaactgtt ctaacccaaatc tgctgactgc aaaacagccg tcaatttttc atctgatccc 840  
gatgcgtgtc tcattacca agctgggttca aagtgatata acaagtgttgg aaggtttgag 900  
cattgcaatt tcaacgacgt cacaaccgc ttgagggaaa atgagctaac gtactactgc 960  
tgcaagaagg acctgtgtaa ctttaacgaa cagcttgaaa at 1002

<210> 8  
<211> 334  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 8

Ile	Ser	Cys	Gly	Ser	Pro	Pro	Pro	Ile	Leu	Asn	Gly	Arg	Ile	Ser	Tyr
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Tyr	Ser	Thr	Pro	Ile	Ala	Val	Gly	Thr	Val	Ile	Arg	Tyr	Ser	Cys	Ser
								20					25		30
Gly	Thr	Phe	Arg	Leu	Ile	Gly	Glu	Lys	Ser	Leu	Leu	Cys	Ile	Thr	Lys
								35					40		45
Asp	Lys	Val	Asp	Gly	Thr	Trp	Asp	Lys	Pro	Ala	Pro	Lys	Cys	Glu	Tyr
								50					55		60
Phe	Asn	Lys	Tyr	Ser	Ser	Cys	Pro	Glu	Pro	Ile	Val	Pro	Gly	Gly	Tyr
								65					70		75
Lys	Ile	Arg	Gly	Ser	Thr	Pro	Tyr	Arg	His	Gly	Asp	Ser	Val	Thr	Phe
								85					90		95
Ala	Cys	Lys	Thr	Asn	Phe	Ser	Met	Asn	Gly	Asn	Lys	Ser	Val	Trp	Cys
								100					105		110
Gln	Ala	Asn	Asn	Met	Trp	Gly	Pro	Thr	Arg	Leu	Pro	Thr	Cys	Val	Ser
								115					120		125
Val	Phe	Pro	Leu	Glu	Cys	Pro	Ala	Leu	Pro	Met	Ile	His	Asn	Gly	His
								130					135		140
His	Thr	Ser	Glu	Asn	Val	Gly	Ser	Ile	Ala	Pro	Gly	Leu	Ser	Val	Thr
								145					150		155
Tyr	Ser	Cys	Glu	Ser	Gly	Tyr	Leu	Leu	Val	Gly	Glu	Lys	Ile	Ile	Asn
								165					170		175
Cys	Leu	Ser	Ser	Gly	Lys	Trp	Ser	Ala	Val	Pro	Pro	Thr	Cys	Glu	Glu
								180					185		190
Ala	Arg	Cys	Lys	Ser	Leu	Gly	Arg	Phe	Pro	Asn	Gly	Lys	Val	Lys	Glu
								195					200		205
Pro	Pro	Ile	Leu	Arg	Val	Gly	Val	Thr	Ala	Asn	Phe	Phe	Cys	Asp	Glu
								210					215		220
Gly	Tyr	Arg	Leu	Gln	Gly	Pro	Pro	Ser	Ser	Arg	Cys	Val	Ile	Ala	Gly
								225					230		235
Gln	Gly	Val	Ala	Trp	Thr	Lys	Met	Pro	Val	Cys	Ser	Gly	Gly	Gly	
								245					250		255
Ser	Leu	Gln	Cys	Tyr	Asn	Cys	Pro	Asn	Pro	Thr	Ala	Asp	Cys	Lys	Thr
								260					265		270
Ala	Val	Asn	Cys	Ser	Ser	Asp	Phe	Asp	Ala	Cys	Leu	Ile	Thr	Lys	Ala
								275					280		285
Gly	Leu	Gln	Val	Tyr	Asn	Lys	Cys	Trp	Lys	Phe	Glu	His	Cys	Asn	Phe
								290					295		300
Asn	Asp	Val	Thr	Thr	Arg	Leu	Arg	Glu	Asn	Glu	Leu	Thr	Tyr	Tyr	Cys
								305					310		315
Cys	Lys	Lys	Asp	Leu	Cys	Asn	Phe	Asn	Glu	Gln	Leu	Glu	Asn		
								325					330		

<210> 9  
<211> 1554  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 9

gactgtggcc	ttcccccaga	tgtaccta	at gcccagccag	c ttttggaaagg	ccgtacaagt	60
tttcccgagg	atactgtaat	aacgtacaaa	tgtgaagaaa	gcttttgtaaa	aattcctggc	120
gagaaggact	cagtgtatcg	ccttaaggcc	agtcaatgg	cagatatatg	agagttctgc	180
aatcgtatcg	gcgagggtgc	aacaaggcta	aattctgc	ccctcaaaca	gccttatata	240
actcagaatt	atttccatgt	cggtaatgtt	gttggaaat	atgtgccgtcc	aggttacaga	300
agagaacatt	ctctatcacc	aaaactaact	tgccttcaga	attnaaaatg	gtccacagca	360

gtcgaatttt gtaaaaagaa atcatgcctt aatccgggag aaatacggaa tggtagatt 420  
 gatgtaccag gtggcatatt atttggtgca accatctct tctcatgtaa cacagggtac 480  
 aaattatttg gctcgacttc tagttttgt cttatccat gcagctctgt ccagtggagt 540  
 gaccgttgc cagagtgcag agaaaattat tgcgcacacc caccacaat tgacaatgg 600  
 ataattcaag gggAACGTGA ccattatgg tatagacagt ctgtaacgtt tgcatgtat 660  
 aaaggattca ccatgattgg agagcactt atttattgtt ctgtgaataa tgatgaaggg 720  
 gagtggagtg gcccaccacc tgaatgcaga tcctctggg gcggtggctc gggcggaggt 780  
 gggtcgggtg gcggcgatc catttcttgt ggctctcc cgcctatctt aaatggccgg 840  
 attagttattt attctacccc cattgctgtt ggtaccgtt taaggtacag ttgttcaggt 900  
 accttccgcc tcattggaga aaaaagtcta ttatgcataa ctaaagacaa agtgatgg 960  
 acctggata aacctgctcc taaaatgttatttcaata aatattcttc ttgcccgttag 1020  
 cccatagttc caggaggata caaaaatttgcggatc cttacagaca tggtgattct 1080  
 gtgacatgg cctgtaaaac caacttctcc atgaacggaa acaagtctgt ttgggtgtcaa 1140  
 gcaaaaataa tggggggcc gacacgacta ccaacctgtt taagtgtttt ccctctcgag 1200  
 tgtccagcac ttccatgtatccacaatggatcatcacaatggatgttggctccatt 1260  
 gctccagatgttgc ttacagctgtt gaatctggttt acttgctgtt tgagaaaaag 1320  
 atcattaact gtttgttcc gggaaaatgg agtgctgtcc cccccacatg tgaagaggca 1380  
 cgctgttaat ctctaggacg atttccaaat gggaaaggtaa aggagcccttcc aatttccgg 1440  
 gttgggttaa ctgcaaaactt ttctgttgc ttgggttgcactgcaagg cccaccttct 1500  
 agtcgggtgtt taatttgcgtt acaggagttt gcttggacca aaatggccagt atgt 1554

<210> 10

<211> 518

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =

synthetic construct

<400> 10  
 Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu  
 1 5 10 15  
 Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu  
 20 25 30  
 Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys Leu  
 35 40 45  
 Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys  
 50 55 60  
 Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile  
 65 70 75 80  
 Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg  
 85 90 95  
 Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu  
 100 105 110  
 Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Ser  
 115 120 125  
 Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro Gly  
 130 135 140  
 Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly Tyr  
 145 150 155 160  
 Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser Ser  
 165 170 175  
 Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys Pro  
 180 185 190  
 Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp His  
 195 200 205  
 Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe Thr  
 210 215 220  
 Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly

225	230	235	240
Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Ser Ser Gly Gly Gly			
245	250	255	
Ser Gly Gly Gly Ser Gly Gly Gly Ser Ile Ser Cys Gly Ser			
260	265	270	
Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr Tyr Ser Thr Pro Ile			
275	280	285	
Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser Gly Thr Phe Arg Leu			
290	295	300	
Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys Asp Lys Val Asp Gly			
305	310	315	320
Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr Phe Asn Lys Tyr Ser			
325	330	335	
Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr Lys Ile Arg Gly Ser			
340	345	350	
Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe Ala Cys Lys Thr Asn			
355	360	365	
Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys Gln Ala Asn Asn Met			
370	375	380	
Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser Val Phe Pro Leu Glu			
385	390	395	400
Cys Pro Ala Leu Pro Met Ile His Asn Gly His His Thr Ser Glu Asn			
405	410	415	
Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr Tyr Ser Cys Glu Ser			
420	425	430	
Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn Cys Leu Ser Ser Gly			
435	440	445	
Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu Ala Arg Cys Lys Ser			
450	455	460	
Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu Pro Pro Ile Leu Arg			
465	470	475	480
Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu Gly Tyr Arg Leu Gln			
485	490	495	
Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly Gln Gly Val Ala Trp			
500	505	510	
Thr Lys Met Pro Val Cys			
515			

<210> 11  
<211> 990  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 11  
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aagtttgagc attgcaattt caacgacgtc acaaaccgct tgagggaaaa tgagctaacg 180  
tactactgtct gcaagaagga cctgtgttaac tttaacgaac agcttgaaaa ttcctctgg 240  
ggcggtgtggct ccggcgagg tgggtccggt ggcggcggat ccatttcttg tggctctcct 300  
ccgcctatcc taaatggccg gattagttat tattctaccc ccattgtctgt tggtaccgtg 360  
ataaggtaca gttgttcagg taccttccgc ctcattggag aaaaaagttt attatgcata 420  
actaaagaca aagtggatgg aacctggat aaacctgtct ctaaatgtga atatttcaat 480  
aaatatttctt ctgtccctga gccccatagta ccaggaggat aaaaaattag aggctctaca 540  
ccctacagac atggtgattc tgtgacattt gcctgtaaaa ccaacttctc catgaacgga 600  
aacaagtctg tttgtgtca agcaaataat atgtggggc cgacacgact accaacctgt 660  
gtaagtgttt tccctctcga gtgtccagca cttccttatga tccacaatgg acatcacaca 720

agtgagaatg ttggctccat tgctccagga ttgtctgtga cttacagctg tgaatctgg 780  
taccttgcctg ttggagaaaa gatcattaaac tggttgcctt cgggaaaatg gagtgctgtc 840  
ccccccacat gtgaagaggc acgctgtaaa tctctaggac gatcccaa tggaaaggta 900  
aaggagcctc caattctccg gggtgggtga actgcaaaact ttttctgtga tgaagggtat 960  
cgactgcaag gcccacccctc tagtcggtgt 990

<210> 12  
<211> 330  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 12  
Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala  
1 5 10 15  
Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly  
20 25 30  
Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn  
35 40 45  
Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys  
50 55 60  
Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Ser Ser Gly  
65 70 75 80  
Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Ile Ser  
85 90 95  
Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr Tyr Ser  
100 105 110  
Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser Gly Thr  
115 120 125  
Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys Asp Lys  
130 135 140  
Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr Phe Asn  
145 150 155 160  
Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr Lys Ile  
165 170 175  
Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe Ala Cys  
180 185 190  
Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys Gln Ala  
195 200 205  
Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser Val Phe  
210 215 220  
Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His His Thr  
225 230 235 240  
Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr Tyr Ser  
245 250 255  
Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn Cys Leu  
260 265 270  
Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu Ala Arg  
275 280 285  
Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu Pro Pro  
290 295 300  
Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu Gly Tyr  
305 310 315 320  
Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys  
325 330

<210> 13

<211> 5994  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 13

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gagtttccca ttgggacata tctgaactat gaatccgc cttgttattc cgaaagaccg 120  
tttctatca tctgcctaaa aaactcagtc tggactggtg ctaaggacag gtgcagacgt 180  
aaatcatgtc gtaatcctcc agatcctgt aatggcatgg tgcatgtat caaaggcatc 240  
cagttcgat cccaaattaa atattctgt actaaaggat accgactcat tggtcctcg 300  
tctgccacat gcatcatctc aggtgatact gtcatttggg ataatgaaac acctattgt 360  
gacagaattc cttgtggct accccccacc atcacaatg gagatttcat tagcaccaac 420  
agagagaatt ttcactatgg atcagtggtg acctaccgct gcaatcctgg aagcggaggg 480  
agaaagggtt ttgagcttg gggtgagccc tccatatact gcaccagcaa tgacgatcaa 540  
gtgggcatct ggagcggccc cgccccctc tagtgcattatac ctaacaaaatg cacgcctcca 600  
aatgtggaaa atggaatatt ggtatctgac aacagaagct tattttcctt aaatgaagtt 660  
gtggagttt ggtgtcagcc tggctttgtc atgaaaggac cccgcccgtgt gaagtgccag 720  
gccctgaaca aatgggagcc ggagctacca agctgctcca gggtatgtca gccacccctca 780  
gatgtcctgc atgctgagcg tacccaaagg gacaaggaca acttttcacc tgggcaggaa 840  
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ccccagggag actggagccc tgcagcccc acatgtgaag taaaatcctg tgatgacttc 960  
atgggcaac ttcttaatgg ccgtgtgcta ttccacttgc atctccagct tggagcaaaa 1020  
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ttggctggaa tggaaagcct ttggaaatagc agtgttccag tgtgtgaaca aatctttgt 1140  
ccaagtcttc cagttattcc taatgggaga cacacaggaa aacctctgga agtctttccc 1200  
tttggaaaag cagtaaatta cacatgcac ccccacccag acagagggac gagcttcgac 1260  
ctcattggag agagcaccat ccgctgcaca agtgcaccctc aagggatgg ggttggagc 1320  
agccctgccc ctcgctgtgg aattctgggt cactgtcaag ccccagatca ttttctgtt 1380  
gccaagttga aaacccaaac caatgcacatc gactttccca ttgggacatc tttaaagtac 1440  
gaatgccgtc ctgagttacta cgggaggcca ttctctatca catgtctaga taacctggtc 1500  
tggtaagtc ccaaagatgt ctgtaaacgt aaatcatgtc aaactccctc agatccagtg 1560  
aatggcatgg tgcattgtat cacagacatc caggttggat ccagaatcaa ctattctgt 1620  
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acctaccgct gcaatcctgg aagcggaggg agaaagggtt ttgagcttgc ggttgagccc 1860  
tccatatact gcaccagcaa tgacgatcaa gtggcatct ggagcggccc gccccctcgt 1920  
tgcattatac ctaacaaaatg cacgcctcc aatgtggaaa atgaaatatt ggtatctgac 1980  
aacagaagct tattttcctt aaatgaagtt gtggagttt ggtgtcagcc tggctttgtc 2040  
atgaaaggac cccgcccgtgt gaagtgcac gcccctgaaca aatgggagcc ggagctacca 2100  
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 ggagaacacgtt caatatttg caccagcaaa gatgatcaag ttgggttttgg gagcagccct 4620  
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 ctttctgttc ctgtgcctg cccacatcca cccaaagatcc aaaacgggca ttacattgg 5460  
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 atcttcttta ttttactcat cattttcctc tcttggataa ttctaaagca cagaaaaggc 5880  
 aataatgcac atgaaaaccc taaagaagtg gctatccatt tacattctca aggaggcagc 5940  
 agcgttcatc cccgaactct gcaaacaat gaagaaaata gcagggtcct tcct 5994

<210> 14  
 <211> 2048  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 14

Met Cys Leu Gly Arg Met Gly Ala Ser Ser Pro Arg Ser Pro Glu Pro  
 1 5 10 15  
 Val Gly Pro Pro Ala Pro Gly Leu Pro Phe Cys Cys Gly Gly Ser Leu  
 20 25 30  
 Leu Ala Val Val Val Leu Leu Ala Leu Pro Val Ala Trp Gly Gln Cys  
 35 40 45  
 Asn Ala Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr  
 50 55 60  
 Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr  
 65 70 75 80  
 Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu  
 85 90 95  
 Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser  
 100 105 110  
 Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys  
 115 120 125  
 Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr  
 130 135 140  
 Arg Leu Ile Gly Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr  
 145 150 155 160  
 Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly  
 165 170 175  
 Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu  
 180 185 190  
 Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser  
 195 200 205  
 Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys  
 210 215 220  
 Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln  
 225 230 235 240  
 Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile  
 245 250 255  
 Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu  
 260 265 270  
 Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys  
 275 280 285  
 Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg  
 290 295 300  
 Val Cys Gln Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg  
 305 310 315 320  
 Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu  
 325 330 335  
 Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln  
 340 345 350  
 Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp  
 355 360 365  
 Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn  
 370 375 380  
 Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln  
 385 390 395 400  
 Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser  
 405 410 415  
 Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser  
 420 425 430  
 Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val  
 435 440 445  
 Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp  
 450 455 460  
 Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr  
 465 470 475 480  
 Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys

485	490	495
Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys		
500	505	510
Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu		
515	520	525
Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr		
530	535	540
Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg		
545	550	555
Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val		
565	570	575
Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr		
580	585	590
Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly		
595	600	605
Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro		
610	615	620
Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn		
625	630	635
Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro		
645	650	655
Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile		
660	665	670
Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala		
675	680	685
Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn		
690	695	700
Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val		
705	710	715
Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg		
725	730	735
Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys		
740	745	750
Ser Arg Val Cys Gln Pro Pro Asp Val Leu His Ala Glu Arg Thr		
755	760	765
Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser		
770	775	780
Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr		
785	790	795
800		
Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser		
805	810	815
Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro		
820	825	830
Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly		
835	840	845
Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met		
850	855	860
Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys		
865	870	875
880		
Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu		
885	890	895
Glu Val Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His		
900	905	910
915	920	925
930	935	940
945	950	955
960		
Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr		
965	970	975

Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser  
                   980                  985                  990  
 Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys  
                   995                  1000                  1005  
 Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val  
                   1010                  1015                  1020  
 His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys  
                   1025                  1030                  1035                  1040  
 Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu  
                   1045                  1050                  1055  
 Ser Gly Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg  
                   1060                  1065                  1070  
 Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser  
                   1075                  1080                  1085  
 Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys  
                   1090                  1095                  1100  
 Asn Leu Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro  
                   1105                  1110                  1115                  1120  
 Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly  
                   1125                  1130                  1135  
 Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val  
                   1140                  1145                  1150  
 Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn  
                   1155                  1160                  1165  
 Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro  
                   1170                  1175                  1180  
 Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro  
                   1185                  1190                  1195                  1200  
 Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu His Gly Glu  
                   1205                  1210                  1215  
 His Thr Pro Ser His Gln Asp Asn Phe Ser Pro Gly Gln Glu Val Phe  
                   1220                  1225                  1230  
 Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Leu His  
                   1235                  1240                  1245  
 Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val  
                   1250                  1255                  1260  
 Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu  
                   1265                  1270                  1275                  1280  
 Phe Pro Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp  
                   1285                  1290                  1295  
 Glu Gly Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val  
                   1300                  1305                  1310  
 Gly Met Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile  
                   1315                  1320                  1325  
 Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr  
                   1330                  1335                  1340  
 Pro Ser Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp  
                   1345                  1350                  1355                  1360  
 Pro His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr  
                   1365                  1370                  1375  
 Ile Arg Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro  
                   1380                  1385                  1390  
 Ala Pro Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro  
                   1395                  1400                  1405  
 Glu Gln Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu  
                   1410                  1415                  1420  
 Phe Pro Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe  
                   1425                  1430                  1435                  1440  
 Gly Lys Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser  
                   1445                  1450                  1455  
 Val Glu Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Glu Pro

1460	1465	1470
Phe Asn Gly Met Val His Ile Asn Thr Asp Thr Gln Phe	Gly Ser Thr	
1475	1480	1485
Val Asn Tyr Ser Cys Asn Glu Gly Phe Arg Leu Ile	Gly Ser Pro Ser	
1490	1495	1500
Thr Thr Cys Leu Val Ser Gly Asn Asn Val Thr Trp Asp	Lys Lys Ala	
1505	1510	1515
Pro Ile Cys Glu Ile Ile Ser Cys Glu Pro Pro Pro Thr	Ile Ser Asn	
1525	1530	1535
Gly Asp Phe Tyr Ser Asn Asn Arg Thr Ser Phe His Asn	Gly Thr Val	
1540	1545	1550
Val Thr Tyr Gln Cys His Thr Gly Pro Asp Gly Glu Gln	Leu Phe Glu	
1555	1560	1565
Leu Val Gly Glu Arg Ser Ile Tyr Cys Thr Ser Lys Asp	Asp Gln Val	
1570	1575	1580
Gly Val Trp Ser Ser Pro Pro Pro Arg Cys Ile Ser Thr	Asn Lys Cys	
1585	1590	1595
Thr Ala Pro Glu Val Glu Asn Ala Ile Arg Val Pro	Gly Asn Arg Ser	
1605	1610	1615
Phe Phe Ser Leu Thr Glu Ile Ile Arg Phe Arg Cys Gln	Pro Gly Phe	
1620	1625	1630
Val Met Val Gly Ser His Thr Val Gln Cys Gln Thr Asn	Gly Arg Trp	
1635	1640	1645
Gly Pro Lys Leu Pro His Cys Ser Arg Val Cys Gln	Pro Pro Pro Glu	
1650	1655	1660
Ile Leu His Gly Glu His Thr Leu Ser His Gln Asp Asn	Phe Ser Pro	
1665	1670	1675
Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Ser Tyr Asp	Leu Arg Gly	
1685	1690	1695
Ala Ala Ser Leu His Cys Thr Pro Gln Gly Asp Trp Ser	Pro Glu Ala	
1700	1705	1710
Pro Arg Cys Thr Val Lys Ser Cys Asp Asp Phe Leu	Gly Gln Leu Pro	
1715	1720	1725
His Gly Arg Val Leu Leu Pro Leu Asn Leu Gln Leu	Gly Ala Lys Val	
1730	1735	1740
Ser Phe Val Cys Asp Glu Gly Phe Arg Leu Lys Gly	Arg Ser Ala Ser	
1745	1750	1755
His Cys Val Leu Ala Gly Met Lys Ala Leu Trp Asn Ser	Ser Val Pro	
1765	1770	1775
Val Cys Glu Gln Ile Phe Cys Pro Asn Pro Pro Ala	Ile Leu Asn Gly	
1780	1785	1790
Arg His Thr Gly Thr Pro Phe Gly Asp Ile Pro Tyr	Gly Lys Glu Ile	
1795	1800	1805
Ser Tyr Ala Cys Asp Thr His Pro Asp Arg Gly Met	Thr Phe Asn Leu	
1810	1815	1820
Ile Gly Glu Ser Ser Ile Arg Cys Thr Ser Asp Pro	Gln Gly Asn Gly	
1825	1830	1835
Val Trp Ser Ser Pro Ala Pro Arg Cys Glu Leu Ser Val	Pro Ala Ala	
1845	1850	1855
Cys Pro His Pro Pro Lys Ile Gln Asn Gly His Tyr	Ile Gly Gly His	
1860	1865	1870
Val Ser Leu Tyr Leu Pro Gly Met Thr Ile Ser Tyr	Thr Cys Asp Pro	
1875	1880	1885
Gly Tyr Leu Leu Val Gly Lys Gly Phe Ile Phe Cys	Thr Asp Gln Gly	
1890	1895	1900
Ile Trp Ser Gln Leu Asp His Tyr Cys Lys Glu Val Asn	Cys Ser Phe	
1905	1910	1915
Pro Leu Phe Met Asn Gly Ile Ser Lys Glu Leu Glu	Met Lys Lys Val	
1925	1930	1935
Tyr His Tyr Gly Asp Tyr Val Thr Leu Lys Cys Glu	Asp Gly Tyr Thr	

1940	1945	1950
Leu	Glu	Gly
Ser	Pro	Trp
Pro	Trp	Ser
Gln	Cys	Gln
Ala	Asp	Asp
Arg	Trp	Asp
1955	1960	1965
Pro	Pro	Leu
Leu	Ala	Lys
Cys	Thr	Ser
Thr	Ser	Arg
Ala	His	Asp
His	Asp	Ala
Leu	Ile	Val
1970	1975	1980
Gly	Thr	Leu
Leu	Ser	Gly
Gly	Thr	Ile
Ile	Phe	Phe
Ile	Leu	Leu
Ile	Ile	Phe
Ile	Phe	Leu
1985	1990	1995
Ser	Trp	Ile
Ile	Leu	Lys
Lys	His	Arg
Arg	Lys	Gly
Gly	Asn	Asn
Asn	Ala	His
His	Glu	Asn
2005	2010	2015
Pro	Lys	Glu
Glu	Val	Ala
Ala	Ile	His
His	Leu	Ser
Ser	Gln	Gly
Gly	Ser	Ser
Ser	Val	
2020	2025	2030
His	Pro	Arg
Pro	Arg	Thr
Arg	Thr	Leu
Leu	Gln	Thr
Gln	Thr	Asn
Asn	Glu	Glu
Glu	Asn	Ser
Ser	Arg	Val
Arg	Val	Leu
Val	Leu	Pro
2035	2040	2045

<210> 15  
<211> 1029  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 15  
tgtgaggagc caccaacatt tgaagctatg gagctcattt gtaaacaaaa accctactat 60  
gagattgggt aacgagtaga ttataagtgt aaaaaaggat acttcttatat acctcccttt 120  
gccaccata ctatgttgc tcggaatcat acatggctac ctgtctcaga tgacgcctgt 180  
tatagagaaa catgtccata tatacggat cctttaatg gccaaggcagt ccctgcaaat 240  
gggacttaacg agtttggta tcagatgcac tttatttta atgagggta ttacttaatt 300  
ggtgaagaaa ttctatattt tgaacttaaa ggatcgatgt caatattggag cggttaagcccc 360  
ccaatatgtg aaaagggtttt gtgtacacca cctccaaaaa taaaaaatgg aaaacacacc 420  
tttagtgaag tagaagtatt tgagtatctt gatgcgtt cttatagtt tgatcctgca 480  
cctggaccag atccattttc acttatttga gagacacga tttatttgg tgacaattca 540  
gtgtggagtc gtgtgtctcc agagtgtaaa gtggtcaat gtgcattttcc agtagtcgaa 600  
aatggaaaac agatatcagg atttggaaaa aaattttact acaaagcaac agttatgttt 660  
gaatgcata agggtttta cctcgatggc agcgcacacaa ttgtctgtga cagtaacagt 720  
acttgggatc cccaggattcc aaagtgtctt aaagtgtcga cttcttccac tacaaaatct 780  
ccagcgtcca gtgcctcagg tccttaggcct acttacaagc ctccagtc catttatcca 840  
ggatatccta aacctgagga aggaataactt gacagtttg atgtttgggt cattgctgtg 900  
attgttatttgc ccatagttgt tggagttgc gtaatttgc ttgtccctga cagatatctt 960  
caaaggagga agaagaaagg cacataccta actgtatgaga cccacagaga agtaaaaattt 1020  
acttctctc 1029

<210> 16  
<211> 378  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 16  
Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe  
1 5 10 15  
Phe Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe  
. 20 25 30  
Ser Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile  
35 40 45  
Gly Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys

50	55	60
Cys	Lys	Lys
Gly	Tyr	Phe
Tyr	Ile	Pro
Pro	Leu	Ala
Leu	Thr	His
Ala	Thr	Thr
65	70	75
Cys	Asp	Arg
Asn	His	Thr
Trp	Leu	Pro
Val	Ser	Asp
Asp	Ala	Cys
Tyr		
85	90	95
Arg	Glu	Thr
Cys	Pro	Tyr
Ile	Arg	Asp
Pro	Leu	Asn
Gly	Gly	Gln
100	105	110
Pro	Ala	Ala
Asn	Gly	Val
Thr	Tyr	
Glu	Phe	
Tyr	Gly	
Gln		
Met		
His		
Phe		
Ile		
Cys		
115	120	125
Asn	Glu	Gly
Gly	Tyr	Tyr
Tyr	Leu	Ile
Ile	Gly	Glu
Glu	Ile	Leu
Leu	Tyr	Tyr
Tyr	Cys	Glu
Glu		Leu
130	135	140
Lys	Gly	Ser
Ser	Val	Ala
Ala	Ile	Trp
Trp	Ser	Gly
Gly	Lys	Pro
Pro	Pro	Ile
Ile	Cys	Cys
Val	Leu	Thr
Leu	Cys	Pro
Pro	Pro	Pro
Pro	Lys	Ile
Ile	Lys	Asn
Asn	Gly	Gly
Gly	Lys	Lys
His	Thr	Phe
Thr		
145	150	155
Val	Leu	Cys
Cys	Thr	Pro
Pro	Pro	Pro
Pro	Lys	Ile
Ile	Lys	Asn
Asn	Gly	Gly
Gly	Lys	Lys
His	Thr	Phe
Thr		
165	170	175
Ser	Glu	Val
Glu	Val	Phe
Val	Phe	Glu
Glu	Tyr	Tyr
Tyr	Leu	Asp
Asp	Ala	Val
Ala	Val	Thr
Thr	Tyr	Ser
Ser	Cys	
180	185	190
Asp	Pro	Ala
Pro	Gly	Pro
Pro	Asp	Phe
Asp	Ser	Leu
Leu	Ile	Gly
Gly		Glu
195	200	205
Ile	Tyr	Cys
Cys	Gly	Asp
Asp	Asn	Ser
Ser	Val	Trp
Val	Ser	Arg
Arg	Ala	Ala
Ala	Pro	Pro
Pro	Glu	Cys
Cys		
210	215	220
Lys	Val	Val
Val	Lys	Cys
Cys	Arg	Phe
Phe	Pro	Val
Pro	Val	Val
Val	Glu	Asn
Asn	Gly	Gly
Gly	Lys	Lys
Lys	Tyr	Tyr
Tyr	Lys	Ala
Ala	Thr	Thr
Thr	Val	Met
Met	Phe	Glu
Glu		
225	230	235
Ser	Gly	Phe
Phe	Gly	Lys
Gly	Lys	Phe
Lys	Tyr	Tyr
Tyr	Lys	Ala
Ala	Thr	Val
Thr	Val	Met
Met	Phe	Glu
Glu		
245	250	255
Cys	Asp	Lys
Asp	Gly	Phe
Gly	Tyr	Leu
Tyr	Leu	Asp
Asp	Gly	Ser
Gly	Ser	Asp
Ser	Asp	Thr
Asp	Thr	Ile
Thr	Val	Cys
Cys		Asp
260	265	270
Ser	Asn	Ser
Ser	Thr	Trp
Trp	Asp	Pro
Pro	Pro	Val
Val	Pro	Lys
Lys	Cys	Leu
Leu		Lys
275	280	285
Thr	Ser	Thr
Thr	Thr	Lys
Lys	Ser	Pro
Pro	Ala	Ser
Ser	Ser	Ala
Ala	Ser	Ser
Ser	Gly	Pro
Gly	Pro	Arg
290	295	300
Pro	Thr	Tyr
Thr	Lys	Pro
Lys	Pro	Val
Pro	Val	Ser
Ser	Asn	Tyr
Asn	Tyr	Pro
Tyr	Pro	Gly
Pro	Gly	Tyr
Gly	Tyr	Pro
305	310	315
Glu	Glu	Gly
Gly	Ile	Leu
Leu	Asp	Ser
Ser	Leu	Asp
Asp	Val	Val
Val	Trp	Trp
Trp	Val	Val
Val	Ile	Ala
Ala	Val	Val
Val	Ile	Ile
Ile	Ala	Val
325	330	335
Val	Ile	Ala
Ile	Ala	Val
Ala	Val	Gly
Gly	Val	Ala
Ala	Val	Ile
Ile	Cys	Val
Val	Val	Pro
Pro	Tyr	
340	345	350
Arg	Tyr	Leu
Leu	Gln	Arg
Arg	Arg	Arg
Lys	Lys	Lys
Lys	Gly	Thr
Gly	Thr	Tyr
Thr	Tyr	Leu
Leu	Thr	Asp
Asp	Glu	
Glu		
355	360	365
Thr	His	Arg
Arg	Glu	Val
Val	Lys	Phe
Phe	Thr	Ser
Ser	Leu	
370	375	

<210> 17

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 17

Met	Glu	Val	Ser	Ser	Arg	Ser	Ser	Glu	Pro	Leu	Asp	Pro	Val	Trp	Leu
1															15
Leu	Val	Ala	Phe	Gly	Arg	Gly	Gly	Val	Lys	Leu	Glu	Val	Leu	Leu	Leu
															30
Phe	Leu	Leu	Pro	Phe	Thr	Leu	Gly	His	Cys	Pro	Ala	Pro	Ser	Gln	Leu
															45
Pro	Ser	Ala	Lys	Pro	Ile	Asn	Leu	Thr	Asp	Glu	Ser	Met	Phe	Pro	Ile
50															60

Gly Thr Tyr Leu Leu Tyr Glu Cys Leu Pro Gly Tyr Ile Lys Arg Gln  
 65                    70                    75                    80  
 Phe Ser Ile Thr Cys Lys Gln Asp Ser Thr Trp Thr Ser Ala Glu Asp  
 85                    90                    95  
 Lys Cys Ile Arg Lys Gln Cys Lys Thr Pro Ser Asp Pro Glu Asn Gly  
 100                  105                  110  
 Leu Val His Val His Thr Gly Ile Gln Phe Gly Ser Arg Ile Asn Tyr  
 115                  120                  125  
 Thr Cys Asn Gln Gly Tyr Arg Leu Ile Gly Ser Ser Ala Val Cys  
 130                  135                  140  
 Val Ile Thr Asp Gln Ser Val Asp Trp Asp Thr Glu Ala Pro Ile Cys  
 145                  150                  155                  160  
 Glu Trp Ile Pro Cys Glu Ile Pro Pro Gly Ile Pro Asn Gly Asp Phe  
 165                  170                  175  
 Phe Ser Ser Thr Arg Glu Asp Phe His Tyr Gly Met Val Val Thr Tyr  
 180                  185                  190  
 Arg Cys Asn Thr Asp Ala Arg Gly Lys Ala Leu Phe Asn Leu Val Gly  
 195                  200                  205  
 Glu Pro Ser Leu Tyr Cys Thr Ser Asn Asp Gly Glu Ile Gly Val Trp  
 210                  215                  220  
 Ser Gly Pro Pro Pro Gln Cys Ile Glu Leu Asn Lys Cys Thr Pro Pro  
 225                  230                  235                  240  
 Pro Tyr Val Glu Asn Ala Val Met Leu Ser Glu Asn Arg Ser Leu Phe  
 245                  250                  255  
 Ser Leu Arg Asp Ile Val Glu Phe Arg Cys His Pro Gly Phe Ile Met  
 260                  265                  270  
 Lys Gly Ala Ser Ser Val His Cys Gln Ser Leu Asn Lys Trp Glu Pro  
 275                  280                  285  
 Glu Leu Pro Ser Cys Phe Lys Gly Val Ile Cys Arg Leu Pro Gln Glu  
 290                  295                  300  
 Met Ser Gly Phe Gln Lys Gly Leu Gly Met Lys Lys Glu Tyr Tyr Tyr  
 305                  310                  315                  320  
 Gly Glu Asn Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu Glu Gly  
 325                  330                  335  
 Ser Ser Gln Ser Gln Cys Gln Ser Asp Gly Ser Trp Asn Pro Leu Leu  
 340                  345                  350  
 Ala Lys Cys Val Ser Arg Ser Ile Ser Gly Leu Ile Val Gly Ile Phe  
 355                  360                  365  
 Ile Gly Ile Ile Val Phe Ile Leu Val Ile Ile Val Phe Ile Trp Met  
 370                  375                  380  
 Ile Leu Lys Tyr Lys Lys Arg Asn Thr Thr Asp Glu Lys Tyr Lys Glu  
 385                  390                  395                  400  
 Val Gly Ile His Leu Asn Tyr Lys Glu Asp Ser Cys Val Arg Leu Gln  
 405                  410                  415  
 Ser Leu Leu Thr Ser Gln Glu Asn Ser Ser Thr Thr Ser Pro Ala Arg  
 420                  425                  430  
 Asn Ser Leu Thr Gln Glu Val Ser  
 435                  440

<210> 18  
 <211> 232  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 18  
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1	5	10	15												
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
		20				25						30			
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
		35				40						45			
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
		50				55					60				
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Gln	
		65				70				75		80			
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
		85							90			95			
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
		100					105					110			
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
		115					120					125			
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
		130				135					140				
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
		145				150				155		160			
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
		165					170					175			
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Pro	Phe	Phe	Leu	Tyr
		180					185					190			
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
		195				200						205			
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
		210				215					220				
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
		225				230									

<210> 19  
<211> 454.  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 19															
Gly	Ser	Ala	Ser	Ala	Pro	Thr	Leu	Phe	Pro	Leu	Val	Ser	Cys	Glu	Asn
1		5				10						15			
Ser	Pro	Ser	Asp	Thr	Ser	Ser	Val	Ala	Val	Gly	Cys	Leu	Ala	Gln	Asp
							20		25			30			
Phe	Leu	Pro	Asp	Ser	Ile	Thr	Phe	Ser	Trp	Lys	Tyr	Lys	Asn	Asn	Ser
						35		40			45				
Asp	Ile	Ser	Ser	Thr	Arg	Gly	Phe	Pro	Ser	Val	Leu	Arg	Gly	Gly	Lys
					50		55					60			
Tyr	Ala	Ala	Thr	Ser	Gln	Val	Leu	Leu	Pro	Ser	Lys	Asp	Val	Met	Gln
					65		70			75		80			
Gly	Thr	Asp	Glu	His	Val	Val	Cys	Lys	Val	Gln	His	Pro	Asn	Gly	Asn
					85		90					95			
Lys	Glu	Lys	Asn	Val	Pro	Leu	Pro	Val	Ile	Ala	Glu	Leu	Pro	Pro	Lys
					100		105					110			
Val	Ser	Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn	Pro	Arg
					115		120					125			
Ser	Lys	Ser	Lys	Leu	Ile	Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg	Gln
					130		135				140				
Ile	Gln	Val	Ser	Trp	Leu	Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly	Val
					145		150				155			160	

Thr Thr Asp Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr  
                   165                  170                  175  
 Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser  
                   180                  185                  190  
 Gln Ser Met Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln  
                   195                  200                  205  
 Gln Asn Ala Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg  
                   210                  215                  220  
 Val Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser  
                   225                  230                  235                  240  
 Thr Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val  
                   245                  250                  255  
 Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr  
                   260                  265                  270  
 Asn Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu  
                   275                  280                  285  
 Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys  
                   290                  295                  300  
 Thr Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser  
                   305                  310                  315                  320  
 Arg Pro Lys Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro  
                   325                  330                  335  
 Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys  
                   340                  345                  350  
 Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln  
                   355                  360                  365  
 Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met  
                   370                  375                  380  
 Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr  
                   385                  390                  395                  400  
 Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val  
                   405                  410                  415  
 Ala His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys  
                   420                  425                  430  
 Ser Thr Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp  
                   435                  440                  445  
 Thr Ala Gly Thr Cys Tyr  
                   450

<210> 20  
 <211> 1530  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
       synthetic construct

<400> 20  
 atgggcgccc cgggcctgct cggggtttc ttggctctcg tcgcaccggg ggtcctcg 60  
 atttcttgtg gcttcctcc gcctatcta aatggccgga ttagttatta ttctaccccc 120  
 attgctgttg gtaccgtat aaggtacagt tgttcaggtt ccttccgcct cattggagaa 180  
 aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 240  
 aaatgtgaat attcaataa atattctct tgcctcgac ccatagttacc aggaggatac 300  
 aaaatttagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 360  
 aacttctcca tgaacggaaa caagtctgtt tggtgtcaag caaataatat gtggggccg 420  
 acacgactac caacctgtgt aagtgtttc cctctcgagt gtccagcact tccttatgatc 480  
 cacaatggac atcacacaag tgagaatgtt ggctccattg ctccaggatt gtctgtgact 540  
 tacagctgtg aatctggta cttgcttgc ggagaaaaga tcattaactg tttgtcttcg 600  
 ggaaaaatgga gtgtgtcccc cccccacatgt gaagaggcac gctgtaaatc tctaggacga 660

tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaactt 720  
 ttctgtatcg aagggtatcg actgcaaggc ccacccctca gtcgggtgt aattgctgga 780  
 cagggagttg cttggaccaa aatgccatgt aatggaaa tttttgcctt actgcggccg 840  
 cagtcttaga acaaaaactca cacatgccc ccgtccccag cacctgaact cctgggggga 900  
 ccgtcagtct tcctcttccc cccaaaaacc aaggacaccc tcatgatctc ccggaccct 960  
 gaggtcacat gcgtgggtt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 1020  
 tacgtggacg gcgtggaggt gcataatgcc aagacaaggc cgccggagga gcagtacaac 1080  
 agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1140  
 gagtacaagt gcaaggcttc caacaaagcc ctccctgatcc ccacatcgaaa aaccatctcc 1200  
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccccatc ccggaggag 1260  
 atgaccaaga accaggttcag cctgacctgc ctggtaaaag gcttctatcc cagcgacatc 1320  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctccctg 1380  
 ctggactccg acggctcctt cttcccttat agcaagctca ccgtggacaa gagcaggtgg 1440  
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1500  
 cagaagagcc tctccctgtc cccgggtaaa 1530

<210> 21  
 <211> 510  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 21  
 Met Gly Ala Ala Gly Leu Leu Gly Val Phe Leu Ala Leu Val Ala Pro  
 1 5 10 15  
 Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly  
 20 25 30  
 Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg  
 35 40 45  
 Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu  
 50 55 60  
 Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro  
 65 70 75 80  
 Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val  
 85 90 95  
 Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp  
 100 105 110  
 Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys  
 115 120 125  
 Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro  
 130 135 140  
 Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile  
 145 150 155 160  
  
 His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly  
 165 170 175  
 Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu  
 180 185 190  
 Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro  
 195 200 205  
 Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly  
 210 215 220  
 Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe  
 225 230 235 240  
 Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys  
 245 250 255  
 Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu  
 260 265 270

Glu	Ile	Phe	Cys	Pro	Leu	Arg	Pro	Gln	Ser	Arg	Asp	Lys	Thr	His	Thr
275							280					285			
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
290							295					300			
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
305							310				315				320
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
							325				330				335
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
							340				345				350
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
							355				360				365
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
							370				375				380
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Val	Pro	Ile	Glu	Lys	Thr	Ile	Ser
385							390				395				400
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
							405				410				415
Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
							420				425				430
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
							435				440				445
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
							450				455				460
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
465							470				475				480
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
							485				490				495
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys		
							500				505				510

<210> 22

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 22

Glu	Pro	Arg	Ile	Pro	Lys	Pro	Ser	Thr	Pro	Pro	Gly	Ser	Ser	Cys	Pro
1					5				10					15	
Pro	Gly	Asn	Ile	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys
									20					25	
Pro	Lys	Asp	Ala	Leu	Met	Ile	Ser	Leu	Thr	Pro	Lys	Val	Thr	Cys	Val
									35					40	
Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	His	Val	Ser	Trp	Phe
									50					55	
Val	Asp	Asn	Lys	Glu	Val	His	Thr	Ala	Trp	Thr	Gln	Pro	Arg	Glu	Ala
									65					70	
Gln	Tyr	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Ala	Leu	Pro	Ile	Gln	His
									85					90	
Gln	Asp	Trp	Met	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys
									100					105	
Ala	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly	Arg
									115					120	
Ala	Gln	Thr	Pro	Gln	Val	Tyr	Thr	Ile	Pro	Pro	Pro	Arg	Glu	Gln	Met
									130					135	
Ser	Lys	Lys	Lys	Val	Ser	Leu	Thr	Cys	Leu	Val	Thr	Asn	Phe	Phe	Ser
														140	

145	150	155	160
Glu Ala Ile Ser Val Glu Trp Glu Arg Asn Gly Glu Leu Glu Gln Asp			
165	170	175	
Tyr Lys Asn Thr Pro Pro Ile Leu Asp Ser Asp Gly Thr Tyr Phe Leu			
180	185	190	
Tyr Ser Lys Leu Thr Val Asp Thr Asp Ser Trp Leu Gln Gly Glu Ile			
195	200	205	
Phe Thr Cys Ser Val Val His Glu Ala Leu His Asn His His Thr Gln			
210	215	220	
Lys Asn Leu Ser Arg Ser Pro Gly Lys			
225	230		

<210> 23  
<211> 4860  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 23  
gctctctaca ccctcatcac ccctgctgtt ttgcgaacag acacagaaga gcaaattttg 60  
gtggaggccc atggagacag tactccaaa cagcttgaca tctttgttca tgattttcca 120  
cgaaagcaga aaaccttgtt ccaaaccaga gttagatga atccagcagg aggcatgctt 180  
gtcactccaa ctatagat tccagaaaa gaagttagta cggactccag gcaaaatcaa 240  
tatgtgggtt tgcaagtaac tggtcctcaa gttagattgg aaaaggtggt tctcctttct 300  
taccagagta gctttctgtt tatccagaca gataaaggca tctatacacc agggcttcca 360  
gtactctatc gtgttttttc tatggatcac aacacaagca agatgaacaa aacttgtatt 420  
gtttagtttc agatccaga aggcatctt gtcagttcta attcagttga cctaaacttc 480  
ttctggcctt acaatttacc agaccttgc agtttggga cttggaggat tgtggccaaa 540  
tatgaacatt cccagagaa ttatactgca tattttgtat tcagggaaata tgtgttgc 600  
agctttgaag tccgtctgca accatcagag aagttttttt acattgacgg caatgaaaat 660  
ttccacgtgt ctatcaactgc aaggtagtt tatggagagg aagtggaaagg tgtggccctt 720  
gtcccttttgc gagtagaaat agatgtatc aaaaagagta ttccagactc actcacgaga 780  
attccgatta ttgatggaga tgggaaagca acactaaaaa gagatacatt ccgttctcga 840  
tttccaaatc tcaatgagct tggggcat actctgtatg catctgtAAC agtcatgaca 900  
gaatcagca gtgatatgtt agtgactgag caaagccggca ttcatatgtt ggcatctccc 960  
tatcagatcc acttcacaaa aacccccaaa tatttcaagc caggaatgcc atatgaactg 1020  
acggtgtatg ttaccaaccc ttagggctca ccagctgccc atgtgccagt ggtatcagag 1080  
gcctttcatt ctatggaaac cactttgagt gatgggactg ctaagctcat cctgaacata 1140  
ccattgaatg ctcaaaggct accaatcaact gttagaacta accatggaga cctcccaaga 1200  
gaacgcccagg caacaaagtc catgacagcc atagcctacc aaacccaggagg aggatctgga 1260  
aactatcttc atgttagccat tacatctaca gagattaagc ccggagataa cttacctgtc 1320  
aatttcaatg tgaagggcaa tgcaaattca ctgaagcaga tcaaataattt cacatacctc 1380  
atattgaata aaggaaatgtt ttcaggtt ggcaggcaac ccaggagaga tggggcagaat 1440  
ctggtagacca tgaatctgca tatcactcca gatctcatcc cttcccttccg gtttggct 1500  
tactaccaag tgggaaacaa cgaaatttg tctgggtgg tttgtggat 1560  
acctgcatttgg gaacgttgg tttgtggat gacaatctaa tacaatgcc aggagctgca 1620  
atgaaaatca aatttggaaagg ggatccagggt gctcgggtt gtttgcgtt tttgtggat 1680  
gcagtatatg ttctcaatga taaatataag attagccaag ctaagatatg ggacacaata 1740  
gaaaagatgtt actttggctg tacagctggc agtggccaga ataatctggg tttgtggat 1800  
gatgctggac tggctctgac aaccagcaact aatctcaaca ccaaacagag atcagctgca 1860  
aagtgtcctc agcctgcata tcggaggcg tgcagttctg ttttgcgtt tgacagcaac 1920  
gcaagcaaaat cggcagaattt tcaggatcaa gacccgtt aatgctgtga agatgtcatg 1980  
catgagaacc ccatggggta cacttgcgaa aagcgtgca aatacatcca ggagggagat 2040  
gcttgcgtt tggcttccct tgaatgttgcgtt cgctacatca agggggccat agatgaaaac 2100  
caacgggaga gcgagttgtt tctggcaaga gatgataatg aagatgggtt catagcagat 2160  
agtgatatca tctcaaggtc tgatttcccc aagatgggtt tttgtggctaac aaaggacttg 2220  
accggaggagc ctaacagtca agggatttca agcaagacaa tttgttgcgtt aatggggat 2280

tccatcacaa cctgggtggt gctggctgta agcttacac ccaccaaagg gatctgtgtg 2340  
 gctgaacctt atgaaaataag agtcatgaaa gtctcttca ttgatcttca aatgccatat 2400  
 tcagtagtga agaatgagca ggtggagatt cgagctattc tgccacaacta cgtaaacgag 2460  
 gatatttatg tgcgagtggaa actgttatac aaccgcgcct tctgcagtgc ttccacaaaa 2520  
 ggacaaagat accgacagca gttcccattt aaagccctgt cctccagagc agtaccgtt 2580  
 gtgatagtcc cattagagca aggattgcat gatgttgaga ttaaagcaag tgtccaggaa 2640  
 gcgttgggt cagacgggtg gaggaagaaa ctgaaaagtt tacctgaagg ggtacagaaaa 2700  
 tccattgtga ctattgttaa actggaccca agggcaaaag gagttgggtt aacacagcta 2760  
 gaagtgtatca aagccccaa attagatgac agagtgcctg acacagaaat tgaacccaag 2820  
 attatcatcc aagggtgaccc tggctcttag attattgaaa actcaattga tggaaagtaaa 2880  
 ctcaaccatc tcattatcac tccttctggc tggggggagc aaaatatgat ccgcattggcc 2940  
 gcaccagtttggccaccta ctacctggac accacagagc agtggggagac tctcggcata 3000  
 aatcgcgaga ctgaagctgt caatcagatc gtgactgggt atgcccagca gatgggttac 3060  
 aagaaagcag atcatttccta tgcagcattt acaaaaccgtg catctagttc ttggctaaaca 3120  
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 atcatttgtg gaggtgttag gtggctgtt ctgaacaggc aacaaccaga tggagcgttc 3240  
 aaagaaaatg cccctgtact ttctggaaaca atgcaggggag gaattcaagg tgctgaagaa 3300  
 gaagtatattttaacagcttt cattctgtt gctttttttt aatccaaaac aatctgcaat 3360  
 gactatgtca atagtctaga cagcagcatc aagaaggcca caaattttt actcaaaaaag 3420  
 tatgagaaac tgcaaaggcc ttacactaca gcccctcacag cctatgctt ggctgctgca 3480  
 gaccaactca atgatgacag ggtactcatg gcagcatcaa caggaaggga tcattggaa 3540  
 gaatacaatg ctcacacccca caacatttgg ggcacttctt atgccttgg ggcctgctg 3600  
 aaaatgaaga aatttgcata aactgggttttcc atagtcagat ggctgacaga tcagaatttt 3660  
 tatggggaaa catatggaca aaccccaagca acagttatgg catttcaagc tcttgcgtaa 3720  
 tatgagattt agatgcctac ccataaggac ttaaacttag atattactat tgaactgcca 3780  
 gatecgagaag tacctataag gtacagaattt aatttgcata aatctcttgg ggctcgac 3840  
 gtagagacca aactcaacca agacatcaact gtgacagcat caggtgttgg aaaagcaaca 3900  
 atgaccattt tgacattcta taacgcacag ttgcaggaga aggcaaatgt ttgcaataaa 3960  
 ttcatctta atggttctgt tgaaaacatc cacttgcata atatattat tgaactgcca 4020  
 ctcatgtca agatctgcac aaggatcttgg ggagaagttt attctacaat gacaataatt 4080  
 gatatttcta tgctgactgg ttttctccct gatgttgcata accttacaat gctttctaaa 4140  
 ggagtgacca gatacatctc cagatgttgg gttgacaata atatggctca gaaagtagct 4200  
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 aatcttagatg aaaaatgtac caagttctac catccagata aaggaacacagg ccttctcaat 4380  
 aagatatgtt ttggtaacgt ttgcgttgcgt gcaggagaaa cctgttctc gctcaaccat 4440  
 caggaaagga ttgtatgttcc attacaaattt gaaaaagcctt gcgagacgaa tggattt 4500  
 gtctacaaaa ccaagctgtc tcgaatagaa gaacaagatg gtaatgtat ctatgtcatg 4560  
 gatgttttag aagttttaa acaaggatctt gacgaaaatc cacgagcaaa gaccaccac 4620  
 tacataagtc aaaggaaatg ccaggaggtt ctgaatcttca aggtgtatgt tgattatctg 4680  
 atctgggtt ccaggaggtt cctgttgcctt acgaaaagata aaatttcttca catcattaca 4740  
 aagaacacat ggattgagag atggccacat gaagacgaat gtcaggaaaga agaattccaa 4800  
 aagttgttg atgactttgc tcaatgttgc tacacatttttgc tggccctact 4860

<210> 24  
 <211> 1620  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 24  
 Ala Leu Tyr Thr Leu Ile Thr Pro Ala Val Leu Arg Thr Asp Thr Glu  
 1 5 10 15  
 Glu Gln Ile Leu Val Glu Ala His Gly Asp Ser Thr Pro Lys Gln Leu  
 . 20 25 30  
 Asp Ile Phe Val His Asp Phe Pro Arg Lys Gln Lys Thr Leu Phe Gln  
 35 40 45

Thr Arg Val Asp Met Asn Pro Ala Gly Gly Met Leu Val Thr Pro Thr  
       50                    55                    60  
 Ile Glu Ile Pro Ala Lys Glu Val Ser Thr Asp Ser Arg Gln Asn Gln  
       65                    70                    75                    80  
 Tyr Val Val Val Gln Val Thr Gly Pro Gln Val Arg Leu Glu Lys Val  
       85                    90                    95  
 Val Leu Leu Ser Tyr Gln Ser Ser Phe Leu Phe Ile Gln Thr Asp Lys  
       100                   105                   110  
 Gly Ile Tyr Thr Pro Gly Ser Pro Val Leu Tyr Arg Val Phe Ser Met  
       115                   120                   125  
 Asp His Asn Thr Ser Lys Met Asn Lys Thr Val Ile Val Glu Phe Gln  
       130                   135                   140  
 Thr Pro Glu Gly Ile Leu Val Ser Ser Asn Ser Val Asp Leu Asn Phe  
       145                   150                   155                   160  
 Phe Trp Pro Tyr Asn Leu Pro Asp Leu Val Ser Leu Gly Thr Trp Arg  
       165                   170                   175  
 Ile Val Ala Lys Tyr Glu His Ser Pro Glu Asn Tyr Thr Ala Tyr Phe  
       180                   185                   190  
 Asp Val Arg Lys Tyr Val Leu Pro Ser Phe Glu Val Arg Leu Gln Pro  
       195                   200                   205  
 Ser Glu Lys Phe Phe Tyr Ile Asp Gly Asn Glu Asn Phe His Val Ser  
       210                   215                   220  
 Ile Thr Ala Arg Tyr Leu Tyr Gly Glu Glu Val Glu Gly Val Ala Phe  
       225                   230                   235                   240  
 Val Leu Phe Gly Val Lys Ile Asp Asp Ala Lys Lys Ser Ile Pro Asp  
       245                   250                   255  
 Ser Leu Thr Arg Ile Pro Ile Ile Asp Gly Asp Gly Lys Ala Thr Leu  
       260                   265                   270  
 Lys Arg Asp Thr Phe Arg Ser Arg Phe Pro Asn Leu Asn Glu Leu Val  
       275                   280                   285  
 Gly His Thr Leu Tyr Ala Ser Val Thr Val Met Thr Glu Ser Gly Ser  
       290                   295                   300  
 Asp Met Val Val Thr Glu Gln Ser Gly Ile His Ile Val Ala Ser Pro  
       305                   310                   315                   320  
 Tyr Gln Ile His Phe Thr Lys Thr Pro Lys Tyr Phe Lys Pro Gly Met  
       325                   330                   335  
 Pro Tyr Glu Leu Thr Val Tyr Val Thr Asn Pro Asp Gly Ser Pro Ala  
       340                   345                   350  
 Ala His Val Pro Val Val Ser Glu Ala Phe His Ser Met Gly Thr Thr  
       355                   360                   365  
 Leu Ser Asp Gly Thr Ala Lys Leu Ile Leu Asn Ile Pro Leu Asn Ala  
       370                   375                   380  
 Gln Ser Leu Pro Ile Thr Val Arg Thr Asn His Gly Asp Leu Pro Arg  
       385                   390                   395                   400  
 Glu Arg Gln Ala Thr Lys Ser Met Thr Ala Ile Ala Tyr Gln Thr Gln  
       405                   410                   415  
 Gly Gly Ser Gly Asn Tyr Leu His Val Ala Ile Thr Ser Thr Glu Ile  
       420                   425                   430  
 Lys Pro Gly Asp Asn Leu Pro Val Asn Phe Asn Val Lys Gly Asn Ala  
       435                   440                   445  
 Asn Ser Leu Lys Gln Ile Lys Tyr Phe Thr Tyr Leu Ile Leu Asn Lys  
       450                   455                   460  
 Gly Lys Ile Phe Lys Val Gly Arg Gln Pro Arg Arg Asp Gly Gln Asn  
       465                   470                   475                   480  
 Leu Val Thr Met Asn Leu His Ile Thr Pro Asp Leu Ile Pro Ser Phe  
       485                   490                   495  
 Arg Phe Val Ala Tyr Tyr Gln Val Gly Asn Asn Glu Ile Val Ala Asp  
       500                   505                   510  
 Ser Val Trp Val Asp Val Lys Asp Thr Cys Met Gly Thr Leu Val Val  
       515                   520                   525  
 Lys Gly Asp Asn Leu Ile Gln Met Pro Gly Ala Ala Met Lys Ile Lys

530	535	540
Leu Glu Gly Asp Pro Gly Ala Arg Val Gly Leu Val Ala Val Asp Lys		
545	550	555
Ala Val Tyr Val Leu Asn Asp Lys Tyr Lys Ile Ser Gln Ala Lys Ile		
565	570	575
Trp Asp Thr Ile Glu Lys Ser Asp Phe Gly Cys Thr Ala Gly Ser Gly		
580	585	590
Gln Asn Asn Leu Gly Val Phe Glu Asp Ala Gly Leu Ala Leu Thr Thr		
595	600	605
Ser Thr Asn Leu Asn Thr Lys Gln Arg Ser Ala Ala Lys Cys Pro Gln		
610	615	620
Pro Ala Asn Arg Arg Arg Ser Ser Val Leu Leu Leu Asp Ser Asn		
625	630	635
Ala Ser Lys Ala Ala Glu Phe Gln Asp Gln Asp Leu Arg Lys Cys Cys		
645	650	655
Glu Asp Val Met His Glu Asn Pro Met Gly Tyr Thr Cys Glu Lys Arg		
660	665	670
Ala Lys Tyr Ile Gln Glu Gly Asp Ala Cys Lys Ala Ala Phe Leu Glu		
675	680	685
Cys Cys Arg Tyr Ile Lys Gly Val Arg Asp Glu Asn Gln Arg Glu Ser		
690	695	700
Glu Leu Phe Leu Ala Arg Asp Asp Asn Glu Asp Gly Phe Ile Ala Asp		
705	710	715
Ser Asp Ile Ile Ser Arg Ser Asp Phe Pro Lys Ser Trp Leu Trp Leu		
725	730	735
Thr Lys Asp Leu Thr Glu Glu Pro Asn Ser Gln Gly Ile Ser Ser Lys		
740	745	750
Thr Met Ser Phe Tyr Leu Arg Asp Ser Ile Thr Thr Trp Val Val Leu		
755	760	765
Ala Val Ser Phe Thr Pro Thr Lys Gly Ile Cys Val Ala Glu Pro Tyr		
770	775	780
Glu Ile Arg Val Met Lys Val Phe Phe Ile Asp Leu Gln Met Pro Tyr		
785	790	795
Ser Val Val Lys Asn Glu Gln Val Glu Ile Arg Ala Ile Leu His Asn		
805	810	815
Tyr Val Asn Glu Asp Ile Tyr Val Arg Val Glu Leu Leu Tyr Asn Pro		
820	825	830
Ala Phe Cys Ser Ala Ser Thr Lys Gly Gln Arg Tyr Arg Gln Gln Phe		
835	840	845
Pro Ile Lys Ala Leu Ser Ser Arg Ala Val Pro Phe Val Ile Val Pro		
850	855	860
Leu Glu Gln Gly Leu His Asp Val Glu Ile Lys Ala Ser Val Gln Glu		
865	870	875
Ala Leu Trp Ser Asp Gly Val Arg Lys Lys Leu Lys Val Val Pro Glu		
885	890	895
Gly Val Gln Lys Ser Ile Val Thr Ile Val Lys Leu Asp Pro Arg Ala		
900	905	910
Lys Gly Val Gly Gly Thr Gln Leu Glu Val Ile Lys Ala Arg Lys Leu		
915	920	925
Asp Asp Arg Val Pro Asp Thr Glu Ile Glu Thr Lys Ile Ile Ile Gln		
930	935	940
Gly Asp Pro Val Ala Gln Ile Ile Glu Asn Ser Ile Asp Gly Ser Lys		
945	950	955
Leu Asn His Leu Ile Ile Thr Pro Ser Gly Cys Gly Glu Gln Asn Met		
965	970	975
Ile Arg Met Ala Ala Pro Val Ile Ala Thr Tyr Tyr Leu Asp Thr Thr		
980	985	990
Glu Gln Trp Glu Thr Leu Gly Ile Asn Arg Arg Thr Glu Ala Val Asn		
995	1000	1005
Gln Ile Val Thr Gly Tyr Ala Gln Gln Met Val Tyr Lys Lys Ala Asp		

1010	1015	1020
His Ser Tyr Ala Ala Phe Thr Asn Arg Ala Ser	Ser Ser Trp Leu Thr	
1025	1030	1035
Ala Tyr Val Val Lys Val Phe Ala Met Ala Ala Lys	Met Val Ala Gly	1040
1045	1050	1055
Ile Ser His Glu Ile Ile Cys Gly Gly Val Arg Trp	Leu Ile Leu Asn	
1060	1065	1070
Arg Gln Gln Pro Asp Gly Ala Phe Lys Glu Asn Ala	Pro Val Leu Ser	
1075	1080	1085
Gly Thr Met Gln Gly Gly Ile Gln Gly Ala Glu Glu	Val Val Tyr Leu	
1090	1095	1100
Thr Ala Phe Ile Leu Val Ala Leu Leu Glu Ser Lys	Thr Ile Cys Asn	
1105	1110	1115
Asp Tyr Val Asn Ser Leu Asp Ser Ser Ile Lys Lys	Ala Thr Asn Tyr	1120
1125	1130	1135
Leu Leu Lys Lys Tyr Glu Lys Leu Gln Arg Pro Tyr	Thr Thr Ala Leu	
1140	1145	1150
Thr Ala Tyr Ala Leu Ala Ala Asp Gln Leu Asn Asp	Asp Arg Val	
1155	1160	1165
Leu Met Ala Ala Ser Thr Gly Arg Asp His Trp Glu	Glu Tyr Asn Ala	
1170	1175	1180
His Thr His Asn Ile Glu Gly Thr Ser Tyr Ala Leu	Leu Ala Leu Leu	
1185	1190	1195
Lys Met Lys Lys Phe Asp Gln Thr Gly Pro Ile Val	Arg Trp Leu Thr	1200
1205	1210	1215
Asp Gln Asn Phe Tyr Gly Glu Thr Tyr Gly Gln Thr	Gln Ala Thr Val	
1220	1225	1230
Met Ala Phe Gln Ala Leu Ala Glu Tyr Glu Ile Gln	Met Pro Thr His	
1235	1240	1245
Lys Asp Leu Asn Leu Asp Ile Thr Ile Glu Leu Pro	Asp Arg Glu Val	
1250	1255	1260
Pro Ile Arg Tyr Arg Ile Asn Tyr Glu Asn Ala Leu	Leu Ala Arg Thr	
1265	1270	1275
Val Glu Thr Lys Leu Asn Gln Asp Ile Thr Val Thr	Ala Ser Gly Asp	1280
1285	1290	1295
Gly Lys Ala Thr Met Thr Ile Leu Thr Phe Tyr Asn	Ala Gln Leu Gln	
1300	1305	1310
Glu Lys Ala Asn Val Cys Asn Lys Phe His Leu Asn	Val Ser Val Glu	
1315	1320	1325
Asn Ile His Leu Asn Ala Met Gly Ala Lys Gly	Ala Leu Met Leu Lys	
1330	1335	1340
Ile Cys Thr Arg Tyr Leu Gly Glu Val Asp Ser Thr	Met Thr Ile Ile	
1345	1350	1355
Asp Ile Ser Met Leu Thr Gly Phe Leu Pro Asp Ala	Glu Asp Leu Thr	
1365	1370	1375
Arg Leu Ser Lys Gly Val Asp Arg Tyr Ile Ser Arg	Tyr Glu Val Asp	
1380	1385	1390
Asn Asn Met Ala Gln Lys Val Ala Val Ile Ile	Tyr Leu Asn Lys Val	
1395	1400	1405
Ser His Ser Glu Asp Glu Cys Leu His Phe Lys Ile	Leu Lys His Phe	
1410	1415	1420
Glu Val Gly Phe Ile Gln Pro Gly Ser Val Lys Val	Tyr Ser Tyr Tyr	
1425	1430	1435
Asn Leu Asp Glu Lys Cys Thr Lys Phe Tyr His Pro	Asp Lys Gly Thr	1440
1445	1450	1455
Gly Leu Leu Asn Lys Ile Cys Ile Gly Asn Val Cys	Arg Cys Ala Gly	
1460	1465	1470
Glu Thr Cys Ser Ser Leu Asn His Gln Glu Arg Ile	Asp Val Pro Leu	
1475	1480	1485
Gln Ile Glu Lys Ala Cys Glu Thr Asn Val Asp Tyr	Val Tyr Lys Thr	

1490	1495	1500
Lys Leu Leu Arg Ile Glu Glu Gln Asp Gly Asn Asp Ile Tyr Val Met		
1505	1510	1515
Asp Val Leu Glu Val Ile Lys Gln Gly Thr Asp Glu Asn Pro Arg Ala		
1525	1530	1535
Lys Thr His Gln Tyr Ile Ser Gln Arg Lys Cys Gln Glu Ala Leu Asn		
1540	1545	1550
Leu Lys Val Asn Asp Asp Tyr Leu Ile Trp Gly Ser Arg Ser Asp Leu		
1555	1560	1565
Leu Pro Thr Lys Asp Lys Ile Ser Tyr Ile Ile Thr Lys Asn Thr Trp		
1570	1575	1580
Ile Glu Arg Trp Pro His Glu Asp Glu Cys Gln Glu Glu Phe Gln		
1585	1590	1595
Lys Leu Cys Asp Asp Phe Ala Gln Phe Ser Tyr Thr Leu Thr Glu Phe		
1605	1610	1615
Gly Cys Pro Thr		
1620		

<210> 25  
<211> 3039  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 25  
atttcttg gcttcctcc gccttatccta aatggccgga ttagttatta ttctacccccc 60  
attgctgtt gtaaccgtat aaggtagt aaggtacagt tgttcaggta ccttccgcct cattggagaa 120  
aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180  
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagttacc aggaggatac 240  
aaaatttagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaaacc 300  
aacttctcca tgaacggaaa caagtctgtt tggtgtcaag caaataatat gtgggggccc 360  
acacgactac caaacctgtgt aagtgtttc cctctcgagt gtccagcaact tcctatgatc 420  
cacaatggac atcacacaag tgagaatgtt ggctccattt ctccaggatt gtctgtgact 480  
tacagctgtg aatctgttta cttgtttttt ggagaaaaga tcattaaactg tttgtcttcg 540  
ggaaaaatgga gtgtgtccccc cccccacatgt gaagaggcac gctgtaaatc tctaggacga 600  
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttgggtgtaaac tgcaaacttt 660  
ttctgtgtatg aagggtatcg actgcaaggc ccacccctcta gtcgggtgtt aattgctgga 720  
cagggagttt cttggaccaa aatgccagta tgtgaagaaa ttttttgcctt atcacctccc 780  
cctattctca atgaaagaca tataggcaac tcactagcaa atgtctcata tggaagcata 840  
gtcaacttaca cttgtgaccc ggacccagag gaaggagtga acttcatccct tattggagag 900  
agcactctcc gttgtacagt tgatagtcag aagactggga cctggagtgg ccctggccca 960  
cgctgtgaac ttcttacttc tgcggttcag tgtccacatccc cccagatctt aagaggccga 1020  
atggtatctg ggcagaaaaga tcgatatacc tataacgaca ctgtgtatatt tgcttgcatg 1080  
tttggcttca cttgtgaggg cagcaagca atccgatgc atgcccagg cacatgggag 1140  
ccatctgcac cagtcgtgtaa agaaggatgc caggccccctc ctaacatccct caatgggcaa 1200  
aaggaagata gacacatggt cgcgtttgac ccttggaaatcatcttataaata tagtgtaaac 1260  
cctggctatg tgctgggtgg agaagaatcc atacagtgtt cctctgaggg ggtgtggaca 1320  
ccccctgtac cccaaatgca agtggcagcg tggtaagcta caggaaggca actcttgaca 1380  
aaaccccaagc accaatttgt tagaccagat gtcaacttctt cttgtggta agggtacaag 1440  
ttaagtggga gtgtttatca ggagtgtcaa ggcacaaatcc cttgggtttat ggagattcgt 1500  
ctttgttaaag aaatcacctg cccaccaccc cctgttatct acaatggggc acacaccggg 1560  
agttccttag aagattttcc atatggaaacc acggtcactt acacatgtaa ccctggggcca 1620  
gaaagaggag tggaaattcag cctcatttggaa gagaccca tccgttgc aagcaatgt 1680  
caagaaagag gcacctggag tggccctgtt cccctatgtt aactttccct ccttgcgttc 1740  
cagtgcgtcac atgtccatat tgcaaatggaa tacaagatattt ctggcaagga agccccatata 1800  
ttctacaatg acactgtgtac attcaagtgtt tatagtggat ttactttgaa gggcagttgt 1860  
cagattcgtt gcaagctga taacacctgg gatcctgaaa taccagttt tgaaaaagaa 1920

acatgccagc atgtgagaca gagtctcaa gaacttccag ctggttcacg tgtggagcta 1980  
 gttataacgt cctgccaaga tgggtaccag ttgactggac atgcttatca gatgtgtcaa 2040  
 gatgctaaaa atgaaatttg gttcaaaaaag attccacttt gtaaagttat tcactgtcac 2100  
 cctccaccag tgattgtcaa tgggaagcac acaggatga tggcagaaaa ctttctatat 2160  
 gaaaaatgaag tctttatga atgtgaccaa ggattctatc tcctggaga gaaaaaattg 2220  
 cagtgcagaa gtgattctaa aggacatgga tcttgagcg ggccttcccc acagtgccta 2280  
 cgatctcctc ctgtgactcg ctgcctaat ccagaagtca aacatggta caagctcaat 2340  
 aaaacacatt ctgcatattc ccacaatgac atagtgtatg ttgactgcaa tcctggcttc 2400  
 atcatgaatg gtatgcgcgt gattagggt catactgata acacatgggt gccaggtgtg 2460  
 ccaacttgta tgaaaaaagc cttcataggg tgtccacctc cgcctaagac ccctaacggg 2520  
 aaccatactg gtggaaacat agctcgattt tctctggaa tgtcaatcct gtacagctgt 2580  
 gaccaaggct acctgctggt gggagaggca ctccttctt gcacacatga gggAACCTGG 2640  
 agccaaacctg cccctcattt taaagaggtt aactgttagt caccagcaga tatggatgga 2700  
 atccagaaag ggcttggacc aaggaaaatg tatcagtagt gagctgttg aactctggag 2760  
 tgtgaagatg ggtatatgtt ggaaggcagt ccccagagcc agtgcctaatc ggatcaccaa 2820  
 tggAACCTC cccttggcggt ttgcagatcc cgttcaactt ctcctgttct ttgtgttatt 2880  
 gctgcaggtt tgatactt taccttctt attgtcattt ccttatacgt gatataaaaa 2940  
 cacagagaac gcaattatta tacagataca agccagaaaag aagctttca tttagaagca 3000  
 cgagaagtat attctgttga tccataacaac ccagccagc 3039

<210> 26  
 <211> 1033  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 26  
 Met Gly Ala Ala Gly Leu Leu Gly Val Phe Leu Ala Leu Val Ala Pro  
 1 5 10 15  
 Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly  
 20 25 30  
 Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg  
 35 40 45  
 Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu  
 50 55 60  
 Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro  
 65 70 75 80  
 Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val  
 85 90 95  
 Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp  
 . 100 105 110  
 Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys  
 115 120 125  
 Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro  
 130 135 140  
 Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile  
 145 150 155 160  
 His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly  
 165 170 175  
 Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu  
 180 185 190  
 Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro  
 195 200 205  
 Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly  
 210 215 220  
 Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe  
 225 230 235 240  
 Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys

245	250	255
Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu		
260	265	270
Glu Ile Phe Cys Pro Ser Pro Pro Pro Ile Leu Asn Gly Arg His Ile		
275	280	285
Gly Asn Ser Leu Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr		
290	295	300
Cys Asp Pro Asp Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu		
305	310	315
Ser Thr Leu Arg Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser		
325	330	335
Gly Pro Ala Pro Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro		
340	345	350
His Pro Gln Ile Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg		
355	360	365
Tyr Thr Tyr Asn Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr		
370	375	380
Leu Lys Gly Ser Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu		
385	390	395
Pro Ser Ala Pro Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile		
405	410	415
Leu Asn Gly Gln Lys Glu Asp Arg His Met Val Arg Phe Asp Pro Gly		
420	425	430
Thr Ser Ile Lys Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu		
435	440	445
Glu Ser Ile Gln Cys Thr Ser Glu Gly Val Trp Thr Pro Pro Val Pro		
450	455	460
Gln Cys Lys Val Ala Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr		
465	470	475
Lys Pro Gln His Gln Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly		
485	490	495
Glu Gly Tyr Lys Leu Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr		
500	505	510
Ile Pro Trp Phe Met Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro		
515	520	525
Pro Pro Pro Val Ile Tyr Asn Gly Ala His Thr Gly Ser Ser Leu Glu		
530	535	540
Asp Phe Pro Tyr Gly Thr Thr Val Thr Tyr Thr Cys Asn Pro Gly Pro		
545	550	555
Glu Arg Gly Val Glu Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys		
565	570	575
Thr Ser Asn Asp Gln Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu		
580	585	590
Cys Lys Leu Ser Leu Leu Ala Val Gln Cys Ser His Val His Ile Ala		
595	600	605
Asn Gly Tyr Lys Ile Ser Gly Lys Glu Ala Pro Tyr Phe Tyr Asn Asp		
610	615	620
Thr Val Thr Phe Lys Cys Tyr Ser Gly Phe Thr Leu Lys Gly Ser Ser		
625	630	635
Gln Ile Arg Cys Lys Ala Asp Asn Thr Trp Asp Pro Glu Ile Pro Val		
645	650	655
Cys Glu Lys Glu Thr Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu		
660	665	670
Pro Ala Gly Ser Arg Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly		
675	680	685
Tyr Gln Leu Thr Gly His Ala Tyr Gln Met Cys Gln Asp Ala Glu Asn		
690	695	700
Gly Ile Trp Phe Lys Lys Ile Pro Leu Cys Lys Val Ile His Cys His		
705	710	715
Pro Pro Pro Val Ile Val Asn Gly Lys His Thr Gly Met Met Ala Glu		
725	730	735

Asn Phe Leu Tyr Gly Asn Glu Val Ser Tyr Glu Cys Asp Gln Gly Phe  
 740 745 750  
 Tyr Leu Leu Gly Glu Lys Lys Leu Gln Cys Arg Ser Asp Ser Lys Gly  
 755 760 765  
 His Gly Ser Trp Ser Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro  
 770 775 780  
 Val Thr Arg Cys Pro Asn Pro Glu Val Lys His Gly Tyr Lys Leu Asn  
 785 790 795 800  
 Lys Thr His Ser Ala Tyr Ser His Asn Asp Ile Val Tyr Val Asp Cys  
 805 810 815  
 Asn Pro Gly Phe Ile Met Asn Gly Ser Arg Val Ile Arg Cys His Thr  
 820 825 830  
 Asp Asn Thr Trp Val Pro Gly Val Pro Thr Cys Met Lys Lys Ala Phe  
 835 840 845  
 Ile Gly Cys Pro Pro Pro Lys Thr Pro Asn Gly Asn His Thr Gly  
 850 855 860  
 Gly Asn Ile Ala Arg Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys  
 865 870 875 880  
 Asp Gln Gly Tyr Leu Leu Val Gly Glu Ala Leu Leu Leu Cys Thr His  
 885 890 895  
 Glu Gly Thr Trp Ser Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys  
 900 905 910  
 Ser Ser Pro Ala Asp Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg  
 915 920 925  
 Lys Met Tyr Gln Tyr Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly  
 930 935 940  
 Tyr Met Leu Glu Gly Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln  
 945 950 955 960  
 Trp Asn Pro Pro Leu Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val  
 965 970 975  
 Leu Cys Gly, Ile Ala Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val  
 980 985 990  
 Ile Thr Leu Tyr Val Ile Ser Lys His Arg Glu Arg Asn Tyr Tyr Thr  
 995 1000 1005  
 Asp Thr Ser Gln Lys Glu Ala Phe His Leu Glu Ala Arg Glu Val Tyr  
 1010 1015 1020  
 Ser Val Asp Pro Tyr Asn Pro Ala Ser  
 1025 1030

<210> 27  
 <211> 3042  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 27  
 atttcttgc accctcctcc tgaagtcaaa aatgctcgga aaccctatta ttcttcccc 60  
 atagttcctg gaactgttct gaggtacact tgttcaccta gctaccgcct cattggagaa 120  
 aaggctatct tttgtataag tgaaaatcaa gtgcacgcca cctgggataaa agctcctcct 180  
 atatgtaat ctgtgaataa aaccattct tgctcagatc ccatagtacc agggggattc 240  
 atgaataaag gatctaaggc accattcaga catggtgatt ctgtgacatt tacctgtaaa 300  
 gccaacttca ccatgaaagg aagcaaaact gtctggtgcc aggcaaatga aatgtgggga 360  
 ccaacagtc tgccagtctg tgagagtgtat ttcctctgg agtgcctcatt acttccaacg 420  
 attcataatg gacaccacac aggacacat gttgaccagt ttgttgcctgg gttgtctgtg 480  
 acatacagtt gtgaacctgg ctatgtctc actggaaaaa agacaatcaa gtgcttatct 540  
 tcaggagact gggatggtgt catcccgaca tgcaaagagg cccagtgta acatccagga 600  
 aagttccca atggcaggt aaaggaacct ctgagcctc aggtggcac aactgtgtac 660

ttctcctgta atgaagggtta ccaattacaa ggacaaccct ctagtcagtg tgtaattgtt 720  
gaacagaaaag ccatctggac taagaagcca gtatgtaaag aaattctctg cccaccacct 780  
ccacaccttc gtaatggaa tcatacaggc agctttcag aaaatgtacc atatggaaac 840  
acagttaccc acacctgtga cccaaagccc gagaaaggcg tgagcttac tcttattgga 900  
gagaagacta tcaattgtac tactggtagt cagaagactg ggatctggag tggccctgct 960  
ccatattgtg tactttcaac ttctgcagtt ctgtgtttac aaccgaagat caaaagaggg 1020  
caaataattat ctatTTGAA agatagtat tcataataatg acactgtggc attttcttgt 1080  
gaacctgct tcaccttcaa gggcaacagg agcattcgat gcaatgctca tggcacatgg 1140  
gagccacccg taccagtgtg tgaaaaagga tgtagggctc ctcctaaaat tatcaatggg 1200  
caaaaagaag atagttactt gctcaactt gaccctggta catccataag atatagtgt 1260  
gaccctgct atttactggt gggagaggac actatacatt gcaccctgta gggaaagtgg 1320  
acacccatTA cTCCCCAGTG cacagtgtca gagtgtaaac cagtaggacc acatctctt 1380  
aagaggcctc agaatcagtt tattaggaca gctgttaatt cttctgtga tgaagggttc 1440

cagttaaatg agagtgcTTA tcaactgtgt caaggtacaa ttccTTGGTT tataaaaaatc 1500  
cgtcttGTA aagaaaatcac ctgcccacca cttcCTGTta tacacaacgg gacacataca 1560  
tggagttcct cagaagatgt cccatATGGA actgtggta catacatgtg ctatccTGGG 1620  
ccagaggaag gcgtaaaatt caaactcatc ggggagcaaa ccatccactg tacaagtgc 1680  
agcagagggaa gaggcTCTG gagtagccct gctcCTCTC gtaaaacttcc cttcccaGCT 1740  
gtccagtgca cagacgttca tggtaaaat ggagtcaagc tcactgacaa taaagcccc 1800  
tatttctaca atgatagtgt gatgttcaag tggatgtatg gatataattt gagtggaaagc 1860  
agtcagatcc ggtgtaaagc caataatacc tgggatcctg aaaaaccact ttgtaaaaaaaa 1920  
gaaggatgtg agcctatgag agtacatggc cttccagatg attcacatataaaactagt 1980  
aaaagaaccc gtcaaaatgg gtaccaggta actggatata cttatgagaa gtgtcaaaat 2040  
gctgagaatg ggacttgggt taaaaagatt gaagtggta cagttattct ctgtcaacct 2100  
ccaccaaaaa ttgcaaatgg tggtcacaca ggcgtatgg caaagcactt cctatatgg 2160  
aatgaagttt cttatgaatg tgatgaaggg ttctatctt tgggagagaa aagtttgcag 2220  
tgcgtaaatg attctaaagg tcatggctc tggagtggac ctccaccaca atgcttacaa 2280  
tcttctcctc taactcattt ccccgatcca gaagtcaaac atggttacaa actaataaa 2340  
actcattctg cattttctca taatgacata gtacatTTG tctgcaatca aggcttcata 2400  
atgaacggca gccacttgc aagggtgtcat actaataaca catggttacc aggtgtacca 2460  
acttgtatca gaaaggctc tttaggggtg cagtcTCCat ccacaatccc caatggaaat 2520  
catactggtg ggagtatagc tcgattttcc cctggaatgt cagtcatgtc cagttgctac 2580  
caaggctcc ttatggctgg agaggcacgt cttatctgtc ctcatgaggg tacctggagt 2640  
caacctcccc cttttgcaa agaggtaaac tgtagcttcc ctgaagatataaaatgg 2700  
cagaaggat ttcaacctgg gaaaaacctt cgattgggg ctactgtgac tctgaaatgt 2760  
gaggatgggt ataccttgg gggaaagtccc cagagccagt gcccaggatga cagccaaatgg 2820  
aaccctccct tggcttttgc caaataccgt aggtggtaa ctattccctt tatttgggt 2880  
atttctgtgg gctcagcact tattttttgc atgagtgtcg gcttctgtat gatattaaaa 2940  
cacagagaaa gcaattatta tacaagaca agacccaaag aaggagctc tcatttagaa 3000  
acacgagaag tatattctat tgatccatata acccagcaa gc 3042

<210> 28  
<211> 1014  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 28  
Ile Ser Cys Asp Pro Pro Glu Val Lys Asn Ala Arg Lys Pro Tyr  
1 5 10 15  
Tyr Ser Leu Pro Ile Val Pro Gly Thr Val Leu Arg Tyr Thr Cys Ser  
20 25 30  
Pro Ser Tyr Arg Leu Ile Gly Glu Lys Ala Ile Phe Cys Ile Ser Glu  
35 40 45  
Asn Gln Val His Ala Thr Trp Asp Lys Ala Pro Pro Ile Cys Glu Ser  
50 55 60  
Val Asn Lys Thr Ile Ser Cys Ser Asp Pro Ile Val Pro Gly Gly Phe

65	70	75	80
Met Asn Lys Gly Ser	Lys Ala Pro Phe Arg	His Gly Asp Ser Val	Thr
85	90	95	
Phe Thr Cys Lys Ala Asn Phe Thr Met	Lys Gly Ser Lys	Thr Val Trp	
100	105	110	
Cys Gln Ala Asn Glu Met Trp	Gly Pro Thr Ala Leu	Pro Val Cys Glu	
115	120	125	
Ser Asp Phe Pro Leu Glu	Cys Pro Ser Leu Pro	Thr Ile His Asn Gly	
130	135	140	
His His Thr Gly Gln His	Val Asp Gln Phe Val	Ala Gly Leu Ser Val	
145	150	155	160
Thr Tyr Ser Cys Glu Pro	Gly Tyr Leu Leu	Thr Gly Lys Lys Thr Ile	
165	170	175	
Lys Cys Leu Ser Ser Gly Asp	Trp Asp Gly Val Ile	Pro Thr Cys Lys	
180	185	190	
Glu Ala Gln Cys Glu His	Pro Gly Lys Phe Pro Asn	Gly Gln Val Lys	
195	200	205	
Glu Pro Leu Ser Leu Gln Val	Gly Thr Thr Val	Tyr Phe Ser Cys Asn	
210	215	220	
Glu Gly Tyr Gln Leu Gln	Gly Gln Pro Ser Ser	Gln Cys Val Ile Val	
225	230	235	240
Glu Gln Lys Ala Ile Trp	Thr Lys Lys Pro Val	Cys Lys Glu Ile Leu	
245	250	255	
Cys Pro Pro Pro Pro Val	Arg Asn Gly Ser His	Thr Gly Ser Phe	
260	265	270	
Ser Glu Asn Val Pro Tyr	Gly Ser Thr Val	Thr Tyr Thr Cys Asp Pro	
275	280	285	
Ser Pro Glu Lys Gly Val	Ser Phe Thr Leu Ile	Gly Glu Lys Thr Ile	
290	295	300	
Asn Cys Thr Thr Gly Ser	Gln Lys Thr Gly Ile	Trp Ser Gly Pro Ala	
305	310	315	320
Pro Tyr Cys Val Leu Ser	Thr Ser Ala Val	Leu Cys Leu Gln Pro Lys	
325	330	335	
Ile Lys Arg Gly Gln Ile	Leu Ser Ile	Leu Lys Asp Ser Tyr Ser Tyr	
340	345	350	
Asn Asp Thr Val Ala Phe	Ser Cys Glu Pro	Gly Phe Thr Leu Lys Gly	
355	360	365	
Asn Arg Ser Ile Arg Cys	Asn Ala His	Gly Thr Trp Glu Pro Pro Val	
370	375	380	
Pro Val Cys Glu Lys Gly	Cys Gln Ala Pro	Pro Lys Ile Ile Asn Gly	
385	390	395	400
Gln Lys Glu Asp Ser	Tyr Leu Leu Asn	Phe Asp Pro Gly Thr Ser Ile	
405	410	415	
Arg Tyr Ser Cys Asp Pro	Gly Tyr Leu Leu	Val Gly Glu Asp Thr Ile	
420	425	430	
His Cys Thr Pro Glu Gly	Lys Trp Thr Pro Ile	Thr Pro Gln Cys Thr	
435	440	445	
Val Ala Glu Cys Lys	Pro Val Gly Pro His	Leu Phe Lys Arg Pro Gln	
450	455	460	
Asn Gln Phe Ile Arg	Thr Ala Val Asn	Ser Ser Cys Asp Glu Gly Phe	
465	470	475	480
Gln Leu Ser Glu Ser	Ala Tyr Gln Leu	Cys Gln Gly Thr Ile Pro Trp	
485	490	495	
Phe Ile Glu Ile Arg	Leu Cys Lys	Glu Ile Thr Cys Pro Pro Pro	
500	505	510	
Val Ile His Asn Gly	Thr His Thr	Trp Ser Ser Ser Glu Asp Val Pro	
515	520	525	
Tyr Gly Thr Val Val	Thr Tyr Met	Cys Tyr Pro Gly Pro Glu Glu Gly	
530	535	540	
Val Lys Phe Lys Leu Ile	Gly Glu Gln Thr	Ile His Cys Thr Ser Asp	
545	550	555	560

Ser Arg Gly Arg Gly Ser Trp Ser Ser Pro Ala Pro Leu Cys Lys Leu  
                   565                     570                     575  
 Ser Leu Pro Ala Val Gln Cys Thr Asp Val His Val Glu Asn Gly Val  
                   580                     585                     590  
 Lys Leu Thr Asp Asn Lys Ala Pro Tyr Phe Tyr Asn Asp Ser Val Met  
                   595                     600                     605  
 Phe Lys Cys Asp Asp Gly Tyr Ile Leu Ser Gly Ser Ser Gln Ile Arg  
                   610                     615                     620  
 Cys Lys Ala Asn Asn Thr Trp Asp Pro Glu Lys Pro Leu Cys Lys Lys  
                   625                     630                     635                     640  
 Glu Gly Cys Glu Pro Met Arg Val His Gly Leu Pro Asp Asp Ser His  
                   645                     650                     655  
 Ile Lys Leu Val Lys Arg Thr Cys Gln Asn Gly Tyr Gln Leu Thr Gly  
                   660                     665                     670  
 Tyr Thr Tyr Glu Lys Cys Gln Asn Ala Glu Asn Gly Thr Trp Phe Lys  
                   675                     680                     685  
 Lys Ile Glu Val Cys Thr Val Ile Leu Cys Gln Pro Pro Pro Lys Ile  
                   690                     695                     700  
 Ala Asn Gly Gly His Thr Gly Met Met Ala Lys His Phe Leu Tyr Gly  
                   705                     710                     715                     720  
 Asn Glu Val Ser Tyr Glu Cys Asp Glu Gly Phe Tyr Leu Leu Gly Glu  
                   725                     730                     735  
 Lys Ser Leu Gln Cys Val Asn Asp Ser Lys Gly His Gly Ser Trp Ser  
                   740                     745                     750  
 Gly Pro Pro Pro Gln Cys Leu Gln Ser Ser Pro Leu Thr His Cys Pro  
                   755                     760                     765  
 Asp Pro Glu Val Lys His Gly Tyr Lys Leu Asn Lys Thr His Ser Ala  
                   770                     775                     780  
 Phe Ser His Asn Asp Ile Val His Phe Val Cys Asn Gln Gly Phe Ile  
                   785                     790                     795                     800  
 Met Asn Gly Ser His Leu Ile Arg Cys His Thr Asn Asn Thr Trp Leu  
                   805                     810                     815  
 Pro Gly Val Pro Thr Cys Ile Arg Lys Ala Ser Leu Gly Cys Gln Ser  
                   820                     825                     830  
 Pro Ser Thr Ile Pro Asn Gly Asn His Thr Gly Gly Ser Ile Ala Arg  
                   835                     840                     845  
 Phe Pro Pro Gly Met Ser Val Met Tyr Ser Cys Tyr Gln Gly Phe Leu  
                   850                     855                     860  
 Met Ala Gly Glu Ala Arg Leu Ile Cys Thr His Glu Gly Thr Trp Ser  
                   865                     870                     875                     880  
 Gln Pro Pro Pro Phe Cys Lys Glu Val Asn Cys Ser Phe Pro Glu Asp  
                   885                     890                     895  
 Thr Asn Gly Ile Gln Lys Gly Phe Gln Pro Gly Lys Thr Tyr Arg Phe  
                   900                     905                     910  
 Gly Ala Thr Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu Glu Gly  
                   915                     920                     925  
 Ser Pro Gln Ser Gln Cys Gln Asp Asp Ser Gln Trp Asn Pro Pro Leu  
                   930                     935                     940  
 Ala Leu Cys Lys Tyr Arg Arg Trp Ser Thr Ile Pro Leu Ile Cys Gly  
                   945                     950                     955                     960  
 Ile Ser Val Gly Ser Ala Leu Ile Ile Leu Met Ser Val Gly Phe Cys  
                   965                     970                     975  
 Met Ile Leu Lys His Arg Glu Ser Asn Tyr Tyr Thr Lys Thr Arg Pro  
                   980                     985                     990  
 Lys Glu Gly Ala Leu His Leu Glu Thr Arg Glu Val Tyr Ser Ile Asp  
                   995                     1000                     1005  
 Pro Tyr Asn Pro Ala Ser  
                   1010

<211> 1033

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 29

Met Gly Ala Ala Gly Leu Leu Gly Val Phe Leu Ala Leu Val Ala Pro  
1 5 10 15  
Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Val Leu Asn Gly  
20 25 30  
Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg  
35 40 45  
Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu  
50 55 60  
Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro  
65 70 75 80  
Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val  
85 90 95  
Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp  
100 105 110  
Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys  
115 120 125  
Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro  
130 135 140  
Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile  
145 150 155 160  
His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly  
165 170 175  
Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu  
180 185 190  
Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro  
195 200 205  
Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly  
210 215 220  
Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe  
225 230 235 240  
Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys  
245 250 255  
Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu  
260 265 270  
Glu Ile Phe Cys Pro Ser Pro Pro Ile Leu Asn Gly Arg His Ile  
275 280 285  
Gly Asn Ser Leu Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr  
290 295 300  
Cys Asp Pro Asp Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu  
305 310 315 320  
Ser Thr Leu Arg Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser  
325 330 335  
Gly Pro Ala Pro Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro  
340 345 350  
His Pro Gln Ile Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg  
355 360 365  
Tyr Thr Tyr Asn Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr  
370 375 380  
Leu Lys Gly Ser Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu  
385 390 395 400  
Pro Ser Ala Pro Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile  
405 410 415

Leu Asn Gly Gln Lys Glu Asp Arg His Met Val Arg Phe Asp Pro Gly  
                   420                  425                  430  
 Thr Ser Ile Lys Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu  
                   435                  440                  445  
 Glu Ser Ile Gln Cys Thr Ser Glu Gly Val Trp Thr Pro Pro Val Pro  
                   450                  455                  460  
 Gln Cys Lys Val Ala Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr  
                   465                  470                  475                  480  
 Lys Pro Gln His Gln Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly  
                   485                  490                  495  
 Glu Gly Tyr Lys Leu Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr  
                   500                  505                  510  
 Ile Pro Trp Phe Met Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro  
                   515                  520                  525  
 Pro Pro Pro Val Ile Tyr Asn Gly Ala His Thr Gly Ser Ser Leu Glu  
                   530                  535                  540  
 Asp Phe Pro Tyr Gly Thr Thr Val Thr Tyr Thr Cys Asn Pro Gly Pro  
                   545                  550                  555                  560  
 Glu Arg Gly Val Glu Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys  
                   565                  570                  575  
 Thr Ser Asn Asp Gln Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu  
                   580                  585                  590  
 Cys Lys Leu Ser Leu Leu Ala Val Gln Cys Ser His Val His Ile Ala  
                   595                  600                  605  
 Asn Gly Tyr Lys Ile Ser Gly Lys Glu Ala Pro Tyr Phe Tyr Asn Asp  
                   610                  615                  620  
 Thr Val Thr Phe Lys Cys Tyr Ser Gly Phe Thr Leu Lys Gly Ser Ser  
                   625                  630                  635                  640  
 Gln Ile Arg Cys Lys Ala Asp Asn Thr Trp Asp Pro Glu Ile Pro Val  
                   645                  650                  655  
 Cys Glu Lys Glu Thr Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu  
                   660                  665                  670  
 Pro Ala Gly Ser Arg Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly  
                   675                  680                  685  
 Tyr Gln Leu Thr Gly His Ala Tyr Gln Met Cys Gln Asp Ala Glu Asn  
                   690                  695                  700  
 Gly Ile Trp Phe Lys Lys Ile Pro Leu Cys Lys Val Ile His Cys His  
                   705                  710                  715                  720  
 Pro Pro Pro Val Ile Val Asn Gly Lys His Thr Gly Met Met Ala Glu  
                   725                  730                  735  
 Asn Phe Leu Tyr Gly Asn Glu Val Ser Tyr Glu Cys Asp Gln Gly Phe  
                   740                  745                  750  
 Tyr Leu Leu Gly Glu Lys Lys Leu Gln Cys Arg Ser Asp Ser Lys Gly  
                   755                  760                  765  
 His Gly Ser Trp Ser Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro  
                   770                  775                  780  
 Val Thr Arg Cys Pro Asn Pro Glu Val Lys His Gly Tyr Lys Leu Asn  
                   785                  790                  795                  800  
 Lys Thr His Ser Ala Tyr Ser His Asn Asp Ile Val Tyr Val Asp Cys  
                   805                  810                  815  
 Asn Pro Gly Phe Ile Met Asn Gly Ser Arg Val Ile Arg Cys His Thr  
                   820                  825                  830  
 Asp Asn Thr Trp Val Pro Gly Val Pro Thr Cys Met Lys Lys Ala Phe  
                   835                  840                  845  
 Ile Gly Cys Pro Pro Pro Pro Lys Thr Pro Asn Gly Asn His Thr Gly  
                   850                  855                  860  
 Gly Asn Ile Ala Arg Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys  
                   865                  870                  875                  880  
 Asp Gln Gly Tyr Leu Leu Val Gly Glu Ala Leu Leu Leu Cys Thr His  
                   885                  890                  895  
 Glu Gly Thr Trp Ser Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys

900	905	910
Ser Ser Pro Ala Asp Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg		
915	920	925
Lys Met Tyr Gln Tyr Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly		
930	935	940
Tyr Met Leu Glu Gly Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln		
945	950	955
Trp Asn Pro Pro Leu Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val		
965	970	975
Leu Cys Gly Ile Ala Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val		
980	985	990
Ile Thr Leu Tyr Val Ile Ser Lys His Arg Glu Arg Asn Tyr Tyr Thr		
995	1000	1005
Asp Thr Ser Gln Lys Glu Ala Phe His Leu Glu Ala Arg Glu Val Tyr		
1010	1015	1020
Ser Val Asp Pro Tyr Asn Pro Ala Ser		
1025	1030	